

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGCTCTCGGGCTAGT**CATG**GCGTCCCCGTCTCGGAGAC
 TGCAGACTAAACCAGTCATTACTTGTTCAGAGCGTTCTGCTAATCTACACTTTTATTTTC
 TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
 CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG
 TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
 AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTCGAACTGGTCGCTGCCATCGTAGG
 ATTTGTTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
 AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
 TGTGTGGTGTCAACGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
 TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
 ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
 ATTTCCCTTGGAGTTGCTTGCTTCCAAGTATTGGAATCTTCTCGCCTACTGCCWCTCTCG
 TGCCATAACAAATAACCAGTATGAGATAGTG**TAA**CCCAATGTATCTGTGGGCCTATTCTCT
 CTACCTTTAAGGACATTTAGGTCCTCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGACTG
 ACAACACTACTTACTGATAGACCAAAAACTACACCAAGTAGGTTGATTCAATCAAGATGTAT
 GTAGACCTAAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
 TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCTGTTAGATCG
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FIGURE 2

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><MW: -1, pI: 8.36, NX(S/T): 1
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VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTIVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
```

Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGCTGGGCCCGGAGGTAGAGAAAGTCAGT
 GCCACAGCCCCACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
 GCCGGGGTAGGCTCTGGAAGGGGCCCGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCTAGAAGAGGGT
 GTTCCCTCTTCGGGGGTCTCACCAGAAAGAGGTTCTTGGGGGTGCGCCTTCTGAGGAGGGT
 GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG
 GGAATAAGCTCTGCAACTTTCTTTGGCATTAGTTGTTAAAAACAAATAGGATGCAAATTC
 TCAACTCCAGGTTATGAAAACAGTACTTGGAAAACGAAAACACCTAAATGATCGTCTTTG
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
 CACATAGCCCACCTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAAATCCTGTATCTG
 CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG
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 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAATGTGGATGGGCTAGTGTGGACACACT
 GGCAGTAATACGGACTCTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
 GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
 TGATAAGATTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC
 TGTAGCAGAAAACAGATAAAGCTATGATCTTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
 AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKQNVLDGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTTCAGCCCATTGCGC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGTTTCCTAACGGA
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCTGATTAAGATGGTCCATCTACTGGTCTGT
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTCCGAAGC
CTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCTGAGCCTTACGCTGGCCACTGTCAAC
GCCCCTGGCTGGAACCCGACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGAGGTACCAGGCAGCCACCAGGTCCTTCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
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FIGURE 6

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<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

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GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFRIYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCAGATTTTAAAGCCATTCTGCAGTGAATTTCATGAACTAGCAAGAGGACACCATCTT
 CTGTGATTATACAAGAAAGGAGTGTTACCTATCACACAGGGGGAAAA**ATG**CTCTTTTGGGT
 GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAACTAAAGATTGAAG
 ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAAACTTGGCAGCC
 AGAACTTTTGATAAAAAGGGATTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
 AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
 AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGTCTCTGGGGT
 CTGATCAATAATGCTGGTGTTCCCGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGA
 CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC
 CTTTGGTCAAGAAAGCTCAAGGGAGAGTTTATTAATGTCTCCAGTGTTGGAGGTCGCCTTGCA
 ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGAAGGTTTCAATGACAGCTTAAG
 ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA
 ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA
 GACATCAACAACAATATGGAGAAGGTTACATTGAAAAAGTCTAGACAACTGAAAGGCAA
 TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCAGCTCTAACAA
 GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAGATGCCAAATTTTCTGGATACCTCTG
 TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
 TCCCAAGGCAGT**GTA**CTCAGCTAACCCAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
 TTCAAGAACACATCTCCTTTTCAACCCATTCTTATCTGCTCCAACCTGGACTCATTTAGA
 TCGTGCTTATTTGGATTGCAAAAGGGAGTCCACCATCGTGGTGGTATCCAGGGTCCCTG
 CTCAAGTTTTCTTTGAAAGGAGGGCTGGAATGTTACATCACATAGGCAAGTCTGCCCTGT
 ATTTAGGCTTTGCTGCTGGTGTGATGTAAGGGAATTTGAAAGACTTGCCCATTCAAATG
 ATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTACAGTAACTTGTGAATGTT
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FIGURE 8

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LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVS SVGRLAIVGGGYTPSKYAVEGF
NDSLR RDMKAFGVH VSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQY GEGYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTGACGGCGCTGCG**ATG**GCTGCGCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCTCTGACGCCGCCAGTGGCGGGGGCCCTTGGGGCCGTGCGCCACCACT
 GTAGTCATGTACCCACCGCCGCCGCCGCCCTCATCGGACTTCATCTCGGTGACGCTGAG
 CTTTGGCGGAGGCTATTGACAAACAGCAAGAGTTGGCGGGCGCGCTCGTGCTGGAGGAAATGGA
 AGCAACTCTCGAGATTGCAGCGGAATATGATTCTCTCTCTCTGCGCTTCTGCTTTCTGT
 GGACTCCCTCTTACATCAACTTGGCTGACCATTTGGAAAGCTCTGGCTTTCAGGCTTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATGCTGGGTAAAACCAGCAAAATCCACCGCTCTTACCAG
 CTCCTCAGAAGGCGGACACCGACCTGAGAACTTACCTGAGATTTCTGTCACAGAAGACACAA
 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA
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 ATCCGAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCTGAGCAGGGCACCGAG
 CTCCTTCAAGAAGAGCAGAAGTGCCCAACCAAGCTCCCCGCCACGGCCAGGACACAGGG
 CACACAGTGCATCTGAACATATCGCCAGAAGGGCGTGATTGACGCTTCTCTGCATGCATGGA
 AAGGATACCCCAAGTTTGATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTCTCAGT
 GAGTGGTTTGGCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGCT
 GAGGAAAGAAATTTGAGGAAGCCAGGAAGTGGGTGTGGAAGAAGTTACACTTTGAAAGGAGC
 TGGAGCTCAACCTGTTTGAGAGCACGATCCGCATCCTGGGGGGGCTCCTGAGTGCTTACCAC
 CTGTCTGGGGACAGCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC
 CTTCAGAACACCATCCAAGATTCTTACTCGATGTGAACATCGGTACTGGAGTTGCCACCC
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCACTTACGCTGGAGTTCGG
 GAGCTCTCCCGTCTCACAGGGGATAAGAAAGTTTCAGGAGGCAAGTGGAGAAGGTGACACAGCA
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG
 GCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
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 CCGCAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATCTCACACGGGTC
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 GGACCCCTGCC**TAG**GGTGGATGGCTGCTGGTGTGGGACTTCGGGTGGGCAGAGGCACCTTG
 CTGGGTCTGTGGCATTTCCTCAAGGGCCACGTAGCACCGGCAACCGCCAAGTGGCCAGGCT
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 GGCCGCTCAGTCTTGTGTGATGCGGGGTGGGCTGGGCGCGCTGGAGCCTCCGCTGCTTCTC
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 GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGATGGACGCCAGGGGTGCAGC
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FIGURE 10

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IAGLKPANFPVLPAPOKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTOEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTLPSSRAEVPTKPPLPPARTQGTQVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRFSSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEDVDVNLFEISTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
FYSDVNIGTGVAHPPRWTSdstVAEVTISIQLFEFLSRLTGDKKFKQEAQVKTQHIHGLSGK
KDGVLPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLTfVGElaHGRFSakMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPeIVHfNLYPQpGRRDVEVKPADRHNLlRPETVESLFYLYRVTGDRKYQDWG
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AYVFNTEAHPLPIWTPA
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Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGGCGCCGCTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCATGCGCCGC
CGCCTCTCCGCACG**ATG**TCCCCCTCGCGGAGGAAAGCGCGCAGCTGCCCTGGGAGGACGGC
AGGTCCGGGTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGTGGC
CTGCCTCTCGTGCGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
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GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC
CGGGCAGCGCTCATCAACGTGGGCTTCTTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC
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AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGCGGGGGCC
CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCTGGTGACATTC
AGC**TGA**AGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGCCCATATTGCTCAGGCTCAGGA
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FIGURE 12

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RHHIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDDEFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
 GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCT
 CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCCTTCTGTGTCTC
 CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
 GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGCTAGGGGG
 GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
 CCTGTTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGT
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FIGURE 14

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PRGEGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGAGCCGAGCGGACAAAG
 GAGCATGTCCGCGCCGGGGAAAGGCCCGTCTCCGGCCGCCATAAGGGCTCCGGTGC CGCGTGG
 GCCCGCGCCGCGCTCTGCGCCGCCGGCTCCGGGCGCGCCGTGCGCCGCTGCGCCGCGC
 CTCGCCCGCGAGCCCGCGGCCGAGC**ATG**GAGCCACCCGGACGCGCGGGGGCCGCGCGCA
 GCCGCCGTGTTGCTCGCGCTCTCGCTGTTAGCGCTGCTCGCGTGTCTGGGAGCGCGCGCGC
 GCGGCGCGCGCGCGCGCTGCGCCGCCGTGCAAGCACAGCGAGGCGCGCCGAGGGGCTGGC
 AGGGCGCGGGCGCGCCGAGGGCAAGTGGTGTGCAGCAGCCTGGAAGTCTCGCGCAGGTCTCT
 GCCCCAGATACCTCTGCCAACCGCACGGTCACCCCTGATTCTGAGTAACAATAAGATATCCG
 AGCTGAAGAATGGCTCATTTTCTGGGTAAAGTCTCCTTGAAGATTGGACCTCCGAAACAAT
 CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCTCTCTAAAAAGATTGGATCT
 GACAAACAATCGAATAGGATGTCTGAATCGACACATATTTTCGAGGACTCACCAATCTGGTTC
 GGCTAAACCTTTTCGGGAATTTGTTTTCTCATTTATCTCAAGGAACCTTTTGATTATCTTGGC
 TCATTACGGTCTTTGGAATTCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGAT
 GCATCGCTGGGTAAAGGAGAACAATCACGGTACGGGATACCGAGTGTGTTTATCCTAAGT
 CACTGCAGGCCCAACAGTTCACAGCGGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT
 GAATGCGCTCTTTCTACATGACTCCATCTCATCGCCAAGTGTGTTTGAAGGAGACAGCCCT
 TCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTTGTTATCAGGATG
 GGAGAATAGTTGAACCGATGAATCGCAAGGTATTTTTGTTGAAAAGACATGATTCACAAC
 TGCTCCTTGATTGCAAGTGCCCTAACCATTTCTAATATCAGGCTGGATCTACTGGAATTTG
 GGGCTGTGATGTCCAGACCAACGTGGGAATAATACGAGGACTGTGGATATTTGGTATTAG
 AGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTTCAGATGG
 CCCAGAACATTGGCAGCAGTACTGCATATCTGCAGTGTACGCGGAACCCCATGGCAGTGG
 GATATATCCCGGAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGTGGCT
 TTTGGGCAGATGATGATTATTTCTCGCTGTGAGTATGCAAAATGATGTACTAGAGTTCTTTAT
 ATGTTTAATCAGATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGGTTACTGGC
 TTACACTGTGGAAGCAGCCAACCTTTTCTGACAAAATGGATGTTATATTTGTGGCAGAAATGA
 TTGAAAAATTTGAAGATTTACCAAGGAGGAAAAATCAAAGAGCTAGGTGACGTGATGGTT
 GACATTCGAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC
 TAAAGCCTGCAGTAGGATTTGTGAGTGTCTTACGCGCATTGCTACCTACCGGCTAGCCGGTG
 GAGCTCACGTTTTATTCAACATATTACCCAATATTGCTCTGGAAGCTTATGTATCAAGTCT
 ACTGCTTACCGGGATGACCTGTACCCTGTTCCAGAAAGTGGCAGCCTCTGATCGTACAGG
 ACTTTCCGATTATGGGAGGCGGGATCCAGAGGGAACCTGGATAAGCAGCTGAGCTTTAAGT
 GCAATGTTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATCTGCAATCATTT
 AAGACTATTTACAGT**TAA**ATTAGAATGCTCCAATGTTCTGCTTCGCAAAAATAACCTTATTA
 AAAGATTTTTTTTTGCGAAGATAGGTATTATTGCTTTTGTACTGTTTTAAAGAAAACCTA
 ACCAGGAAGAAGTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCTTTTGATTCCCTTT
 CTTCACTAAAAAATACAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAAAATATAC
 ATTGTTACATGTGAAAAAATTTTATTGACTTAAAGTTTATTTATTTGTTTGTGTTTCTCCCT
 GATTTTAAACAATAAGATGTTTTCATGGGCCCTAAAGTATCATGAGCCTTTGGCACTGC
 GCCTGCCAAGCCTAGTGGAGAAGTCAACCTGAGACAGGTGTTTAAATCAAGCAAGCTGTAT
 ATCAAAATTTTGGCAGAAAACACAAATATGTCAATATCTTTTAAAAAAGTATTTCA
 TTGAAGCAAGCAAAATGAAGCATTTTTACTGATTTTTAAATTTGGTGTCTTATAGATATTTT
 GACTACACTGATTGAAGCAATAAGAGGAGGCACAACCTCCAGCACCCTAAGTGAACACATTT
 TTTTCACTTAGCTTTCTGTGGCATGTGTAATTGTATTCTCTGCGGTTTTTAATCTCACAG
 TACTTTATTTCTGTCTTGTCCCTCAATAATATCACAACAATATTCGAGTCATTTTAAATGGC
 TGCATATAACTGATCCAACAGGTGTAGGTGTTCTGTTTAGTGTGACCATCTCAATAATA
 TTGAATGAATGAACGAAAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRGRAQFPLLLLPLSLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSELAQVLPDPTLPNRTVTLLISNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
 FWGLSSSLKRLDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLFQT
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMTF
 SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT
 ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLGAITA
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMPNLN
 TNAVATARQLLAYTVEANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
 VFQKVAASDRITGLSDYGRDPEGNLDKQLSFCNVSNFTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
 433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
 384-390, 403-409, 554-560

CGCTGGGG**ATG**TCTAGGAGCTCGAAGGTGGTGCTGGGCCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAAATTCGAAAAAAGAAAAATTCTGCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAAA
TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTCTTATGGGTTGTTACTGAGAGCACTGCCGAGCTTGTGAGAAGCAGAGGGA
TGGATAGTAGATCCACCTGGTAGTCTGTGACAGTCGGCATGATGACAGGCCAGGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATC

FIGURE 18

MSRSSKVVVLGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

18/249
MSRSSKVVVLGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIIILT
EQLEAEREKMLLAKGSQKS

FIGURE 19

CTGTCGTCTTTGCTTCAGCCGACGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCC
 CAAGTGTGGCTTAATCCGCTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC
 GCTGCCATGCCAGTGACGGTAACCCGACACCACCATCACAAACCACACGAGCTCATCTTCGGG
 CCTGGGGTCCCCATGATCGTGGGGTCCCCCTGGGGCCCTGACACAGCCCTGGGTCTCCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC
 GGGGTCCATGGGCACTGGTCCATGTTACCTGGTGTCTTCTGCTTCTCCGTGACCCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC
 ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCTCTCGGCCCTCCATCATCTACCCACCAC
 CTATGTCCAGTTCCTGTCCACGGCCGTTTCGGGGACACGCCATCGCCGCCACCTTCTTTCT
 CCTGCATCGCGTGTGTGGCTTACGCCACCAGTGGCTTGGACCCGGGGCCCGCCCGCGGAG
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGTGAAGGTGCTGGAGACCTTCGTGCGCTG
 CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCTGCTGAACCTGGGG
 GAGTGCACCAAGTGTACCATCCCCCTCCCCAGCTTCTGTGCGGGCTGGCCTTGCTGTG
 TGTCTCTCTCTATGCCACCGCCCTTGTTCTCTGCCCCCTTACCAGTTCGATGAGAAGTATG
 GCGGCCAGCCTCGGCCTCGAGAGATGTAAGCTGCAGCCGACGCCATGCCTACTACGTGTGT
 GCCTGGGACCGCCAGTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGCCTCTGCCCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCAAGAGGCTCC
 CGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC
 TCCGCTTTCTCTGTGTTTCTCTTCTGCTCCCCCTCCCTCCACCTTTTTCTTTCTTCC
 CAATCTCTGCACTCTAACAGTCTTGGATGCATCTTCTTCTTCCCTTTCTCTTGTGT
 TTCCTTCTGTGTGTTTTGTTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT
 CTTTTCTTCTTTTTTTTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCTCCTGGGTCAAGCGATTCTCCTCC
 CCCAGCCTCCCAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTT
 TTCACCTCTTCTTTTTTCTCATCTCTTTCTGGGTTGCCTGTGCGGCTTCTTATCTGCCTGT
 TTTGCAAGCACCTTCTCTGTGTCTTGGGAGCCCTGAGACTTCTTCTCTCTTGCCTCCA
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACCCCTTGCAGCCGTCCATGCCACAGCCCC
 CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCTCGCTGTGCCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT
 CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCCTTAAATTAAAAACATATATATATATAT
 ATTTGGAGGTCAATAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCCTGGGTCCCTAGG
 CCCCCTTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGCCAGGCTTACAGAACAC
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCACTATTCT
 CTGTGGTATGAAAAAG

FIGURE 20

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTSSSGLSPMIVGSPRALTQPLGLRLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCSVTLLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIAATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPAAEWCAVYAICFILAAIAILLNLGECTNVLPPIFPSPFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFKV

```

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

[illegible]

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKVMHDPNYCHPSTSLHLCS
 LAWSFTRLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSY
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
 PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSSLCSLEDGLLGSPARLASQLLGDE
 LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
 QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
 285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTT
GGCACCCTCCTGCTCAGTGCGACATTGTACACTTAACCCATCTGTTTCTCTAATGCACGA
CAGATTCCTTTACAGACAGGACAACTGTGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAG
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
TACAATCTATTCTTGGCCATCAAGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG
AAGCCTACA**ATGT**TTGGCCTTAGCCAAAATTCGTGATTCCAACGTGTGTTTATTCACTTCT
ATCGGGGAGCCATTGAAAAAGAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT
TTAAAACAATGAAAAATAAACCTATTCTTTGGAAAGTGAAGCAAACCTAAACTCAGATAAA
GAAAAATAACCACCTCAAATCTCAAGGCGAGTCATTCCCTCCTTTGAATCTACCCAACAA
CAGCCACGGAATAACAGATTCTCCAGTAACTCATCAGCAGAGCATTCCTTTGGGCAGTCTAA
AACCCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCCT
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
TGCTCTGTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATA
ACAGTTCATTTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG
ATAGTGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
TCAAGAAAAAACACTCTACAGCCTACCTTAAATTCACCAATAATTCAAACCTCTTTCCAA
ATACGTCAGATCCCCAAAAAGAAAAATAGAAATACAGGAATAGTATTGCGGGCCATTTTAGGT
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGAAAAAGGAAAAC
GGATTCAATTTCCCATCGGCGACTTTATGACGACAGAAATGAACAGTTCTGCGATTAGACA
ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATCTAGCTACTACAATCCAACCTTTGAAT
GATTACGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCATGGATGACATACC
TCCACTTCGTA**CTTCTGTATAGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA
CATCCTAGCCTTTTGACAAATTCATCTTTCAAAAGGTTACACAAAATTAAGTGTACGTTGGAT
TTTGTCAAGGAGAATCATAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
CCAAAGGTTTTCTTCTTACAATTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT
TGTATTTTAGTAGTATTTCTTAGTAGAAAAATTTGTGGAATCAGATAAACTAAAAGATT
TCACCATACAGCCCTGCCTCATACTAAATAATAAAATTTATCCACCAAAAAATCTTAAA
ACAAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
TTTCTTAAATGAAAATTGAAAGGGTCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
GACATAGCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAATGACAGACCTGTATTC
TAGTACGTTATAATTTCTAGATCAGCACACATGATCAGCCCACTGAGTTATGAAGCTGA
CAATGACTGCATTCAACGGGGCCATGGCAGGAAGCTGACCTACCAGGAAAGTAATAGCT
TCTTTAAAGTCTTCAAGGTTTTGGGAATTTAACTTGTCTTAATATATCTTAGGCTTCAA
TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLPNTSDPQKENRNTGIVFGAILGAIL
GVSLLLTVGYLLCGKRKTDSSFHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNDSA
MPSEENARDGIPMDDIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTTGCAGTCTGCAGCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACT**ATG**GTGAAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT
 TCATGCCCAAGAGCACCATTACCCTGGAGAGATGTGCTTTTTGATTCTGAGGATCCTGCA
 AATTCCTTCGTGGAGGAGAGCCTAACTTCTGCCTGTGACTGAGGAGGCTGACATTCGTGA
 GGATGACAACATTGCAATCATTGATGTGCTGTCCCAGTTTCTCTGATAGTGACCCTG³CAG
 CAATTATTATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGCTGGGGAAGTGC
 TATCTGATGCCCCCTCAATACTTCTATTTGTTATGCCTCCAAAAATCTGGTAGAGCTCTTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
 AAGTCCTTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGT
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTACAATATGACTTTAA
 CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
 AAAAAAAGGAAAAAAAAAAAAA²CTACTAACCCTGCAAGCTCTTGTCAAATTTAGTTTAAAT
 TGGCATTGCTTGTTTTTTGAAACTGAAATTACATGAGTTTCATTTTTCTTTGCATTATAG
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCATCC
 GTTGTTTTTTTTGTTTGTGTTTTTCTTTTCTTTTAAAGTAAGCTCTTTATTCATCTTATG
 GTGGAGCAATTTTAAATTTGAAATATTTTAAATGTTTTTGAACTTTTTGTGTAATAATA
 TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTTTCATTTGTACAACCTTCTTGAATTTAGA
 AATTACATCTTTCAGTTCGTGTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
 TTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTTCTCACTACATCTGTATTGTGG
 AATGCACAAAATTTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAA
 CCTATAATAAATTTTACTCTATACAAAAA¹AAAAAAAAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCLMTLLGLSF
 ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
 IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLAGS
 RYLPQTYVVREDLVAVEEIRDVSNLGIIFIYQLCNNRKSFRLRRRDLLGFNKRAIDKCWKIR
 HFPNEFIVETKICQE

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACACGGAAGTCTCT
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTGCGGGGAGCACCCAGTCTGTACGCC
 AAGGAAGTGGTCTGGGGGCACCATGGTTTCGGCGGCAGCCCCAGCCTCCTCATCCTCTGT
 TTGCTGCTGTGGGGTCTGTGCCTGTACCGACGCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGTAGTGGGAGGCCGAGGGCTCGTGGCCTCCTCCCGAGCCTCC
 CGCCACCCTGGACCCCGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAACCTGGGG
 GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA
 TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCTTCCCCAAGAAGAAGTAC
 GTGGACCAGAGTGACCGGGCCGGGGGCCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG
 CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA
 GGGACATGGGGTCCAGTGGAGACACCAGAGGCGCAGGAGGACCGTCTCAGGGGTCTTG
 AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCAG
 GAAGCCAGGGACCAAGTGGGTCCCCCGAAAGCCCTGTGCTGACAGTGTCCACCCAG
 TGCTTAAACAGTCTTCCCGGGCTGCCAGCCCTGACTGTGGGGCCCCAAGTGGTCACCTCCCC
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTGACACTCCCTCCTTGGCCTCCCTGTGG
 TGCCAATCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCGGTGCCCGGA
 GGAATCTTACCAAGTGCCATCATCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
 ACAGTCCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCAAACTACTTTTTAAACA
 GCTACAGGGTAAATCTTCAGCAGCCACTCTGGAATACTGCTCTTAATTTTCTCTGAAGG
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTAAATCCTC
 TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGTACTGCTGCTGG
 GATCAGGTGAATGAATGGAAGTCTTCTGTCTGGCCTCAAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTTGAAGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGAC
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG
 TGTCCACAATATTCGTAGTCTCGACAGGGAGCCTGGGCTCCGTCCTGCTTTAGGGAGGCT
 CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGACAGCTCT
 CCAGGTGCTGAGATATAATGCACAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAPSLILLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPWPWPAL
 SPTSMGFPQPTTLGGPSPPTNFLDGI VDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
 SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
 TRAAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
 GQGELEGSLLLAQEAQGFPVGPPESPCACSSVHPSV

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
 211-217, 238-244, 242-248

[illegible]

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLALLCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALQGQGTREAVGTGVRQVPFGGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPHSGAWETSGGHGIFGSGGGLGGQGGNPGGLGTPWWHGYPGNSAGSFGM
NPQGAFPWQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGGSGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGNSGGSRGDSGSESSW
GSSTGSSSSNHGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRLL
GGSGDNRYRGQSSWGSGGDAVGGVNTVNSETPGMFNFDTFWKNFKSKLGFINWDINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGCGGTGCTCACCG
 TGCCTCGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCTTTGCTGGAATATTACCGGGACATCTTCA
 CTCTCCTGTGCGCTGCACCGGAGCTTGGTGTGTCGAGGAGAGTGAGGGGAGATGTTGTTTCCCTGAACAAG
 TGTGCTACTTCTGCTCTCTGGGCTGGCTTTTCCAGATTCCCAAGTCCCTGAGGACTTGTCTTTCTGGGAAGAGG
 GTCCCTCATATGCTTTGAGGTTGGACACAGTAGGCCCCAGAGCATGGCTTGACAAATGCGCTGTGGTGGACCAAG
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGGAACATGCTCGCTTGTGGGTGTGAGGCATAGTG
 GACGGAGTGGGGCTTTCATGAGGAAATACCCCCACCACTACCACAGCTGGGAGGCCAGCCTTCCAGACCA
 GCCAGGGGCTCGAGGCACAGCTCGCCAGGCCCTTTTCCACACAGCCGCCCTCTTGGCCGGAGCCGTAGAGT
 TCGTGGCAGAAAGAAATTGGATCAAACTGTGTCAACATATCAAGGCTACACTGGTGGCAGATCTGGTGGCCAGG
 CAGAGTCACTTCTCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGAGACCAGCCAGCTGTTGGAGATCT
 TGTGTTCCAGCTGTGCCCTCACGGGGCCAGGCATTTGCCCTGGGGCGGAGATTCTGTCAAGGAAGAGCCCTG
 GGGCTGTGGGGGCTGCTTCCAGAGGAGACCCCGGCAGCCGTTCTGAGCAGTGCAGAGAACATTGCTGTGGGGC
 TTGCAACAGAGAAGGCTGTGCTTGGCTGTACGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAGACAGCAG
 TGAGTGCACACATCTCGAGCCAGGGTCTGAACTGCTGCCCGGGGAGCGGAGGGGCTGCTCCCGGCCCTGAC
 GTGCTCTCTTGGCCGTGGGGCCAGGGACCTGACGAGGGAGTCTCCCAAGGACATCTGGAACAGCTCCTAGGC
 CAGCTGGGGCAGACGCTGCGGTGCGCCAGTTCTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTGCTCTGTG
 GAGTTAGCTTCCCTCTCGTTGCAGATCAAAATCTATCTAGGGCCCCCGCCACAGTACAGGCTGGAGAGACGG
 CAGGCTCGAAGGCTTCTGCACTGCTGCTTTCTTGTGGGAAGGAAGACTTTCAGGGCCGGTTCGCTGCAGCTG
 CTGCTGAGCCCAAGAAATGTGGGGCTTGTGGCAGACACAAGGCCAAGGGATGGGACTTGTGCTATTCTTCTTA
 CGGGAGCTGGTGGGAGAAGGCTGTGATGGGACGGATGGAGATAGAGGCTTGTGCTGGGCACTTCCACAGGCCAG
 TGGCCAGGGGACTTGTGCTGAAGAAATTAGCAACACTGTCTAATCTGTTTCTAGCCAGGCCCCACTCGGCAGAACCC
 CAGCTAAGAGCTGTGAGTTGTGAGGAGTGTGAGCAGCAAAACCGGGGCACTGTGCTGCCCGAGCTAGGGCTGAGAATGGCC
 CTGCTTGGGCTGTGACCAAGAACCTGGACCCCGGCTCACAGGAGGGCCCAAGTGCCCAATGCAAGCCCTCAG
 TGGTTGGGGTGTAGCTGGGTCTACAGTCAAGTCTCTGCTAAGGGTGTCACTGTGCTGGCATCCACACCGCA
 ATCCTAGAGGAAGGAGATTGGCCGTGATTGGGATTTAGGCAGAAAGTCCAGAGATGCCAGTCTCTGGAGTAGAA
 GAGGTGCTGTTTGTATTCTCTTGGATACTAAATGAAATGAGGTGTGTGGGCTTGTGCACACAGAAATTAAGACT
 CATTTGCTATCCAGCATCTCTTAAAACTTTGTAGTCTTGAATTCATGACAGAGGCAAAATGACTCTGCTTAAC
 TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTTATCACCAGGAGCTGGACTCCCATCTCCTT
 ATAAATGCCCTAACACAGCCCGGTCTGTGGCTCATGCTGTAATCCAGCACTTTGAGAGGCTGAGGTGCGGG
 GACTGCTGAGGTGAGGAATTCAAGACCAGCCTGGCCAACTGGCAAAACCCCATCTCTACTAAAAATAAAAAA
 TTATTAGCTGGGCATGGTGTGTGTGCTGTAATCCAGCTACTCAGGAGGATGAGGCAGGAGACTGCTTGAAC
 CTGGAGGTGGAGGTGTCAGTGAGCCGAGGTGCAACCACTGCACTCCAGTCTGGGTAACAGAGCGAGACTTTCTAG
 AAAAAAGCTTAAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCCTCTGACTTCAAGCCCTG
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGACAGGGGCACTTAGAGCTTTTAGAATAAAA
 CTGGTTTTCTTTAAAAAAGGGCTTTTATTAATAATCTCCCAACAGATGGCTCCTGCAATCTGCCACAGCTC
 TGGGCGCTGTCTGTAGGGAAGGCCCTGTTTCCCTGAGGCGGGGCTGGGCTTGTCCATGGGTCCGCGAGCTC
 GCGCTGCTGAGTGGCACCGGGAGCAGCTGTGGCCGTGCTCCTTCYTAGGCAAGTCTTGGGCAAACTAAGCTC
 GGGCCCTTTCTTGAAGAGCCAGGATGGGTGGGTGTGGGGACTCATGGGGAATGGCTGAGGAGTACGTGT
 GAAGAGGGCGCGGTTTGTGGCTGCAGCGGCTCTGAGCGCTCTCTCTGAGCCTCAGTTTCGCTTCCGTTCTA
 ATGAAGAACATGCGCTCTCGGTGTCTCAGGCTATTAGGACTTGCCTCAGGAAGTGGCTTGGACAGGCTCAT
 GTTATTTTCAACAATGCTGCTCGCAGCTTGGCTGGGCAGTCAATGAATGGCCATGTCCCTCTGCTGCTGTGAC
 TGTGCGGCTCGGAGTGTGCGACGACAGGCGGGGCGCAGAGTGTGCCCTGGGGTGAAGGAGGCGCCCGGGAGGG
 CTTCAAGAAAGTGGGCTCCGACCAACAGGACGGCGGGCTCCCGCCGCGCCGCAACACAGCCGTCAGAG
 GCGCGGTAGACAAAGTGGAAGTGGGCTGGGCTGCTGCGCAGCAGGTAGCCCTTGATGCACTGCGGCAGCGG
 TCGTCCCGCAGCTGGAAGCAGCGCCCGTCCACAGCAGCAAGCAGCGGTGCGCCT

FIGURE 32

MCFLNKLLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
 CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP
 SLRRTVEFVAERIGSNVCVKHIKATLVADLVRQAESLLQEQLVTQGEEGGDPAQLEILCSQL
 CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
 IRREVKA AVSRTLRAQGFEPAAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGCTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAAACTG
 AAGACTCTCTGCTTTTGGCCACGACAGTTCTCTGACGCTTCCCTTGAGGTGTGAACCCACATCCC
 TGCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAAATG
 AGTAGCAACAAGAGCAGCGGTGACGAGTGTTCGTGATCCTCTTTGGCCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA
 GCCGCCGACCTGTCAACCTCAAGAAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC
 AACAAGACACTGCCCTCTCGGTGCCACCAGTGTGTGATTGTGACGAGCTCCAGCCACTGTCT
 GGGCACCAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCGTGCGCCATTCC
 AGTGTGTTCCGCGTGTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGT
 CATCTTCTGGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGGGTGTGATCC
 AGCGAGCGGGCTTGGTGTCCCCAACATGGAAGCATATGCCGTCTCTCCCGGCCGATGCGG
 CAATTTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGGAGAAGTCTCATTCGTGGT
 GAGCACAGGTGTTTACCATTGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATG
 GCATGGTCCCCCCTCACTACTGCAGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCCTAC
 TACGAGCCCAAGGGGCCGACGAATGTGTCACTACATCCAGAATGAGCACAGTCGCAAGGG
 CAACCACACCGCTTCATCACCAGAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTATGGCA
 TCACCTTCTCCACCCCTCTTGAGCTTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
 AGGAGAAGCAGCTCCGCCAGCCGCTAGGCCAGGGACCATTCTTGGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
 TGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTTCTGAGTCAATCTG
 AGGCTAAGGACATGTCTTTCCCATGAGGCCTTGGTTCAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTGCCAAGGAGCTGGGAACCTTGGTGTG
 CCCCCTCAATTTCCAGCACAGAAAAGAGAGATTGTGTGGGGTAGAAGCTGTCTGGAGGCC
 GGCCAGAGAATTTGTGGGGTTGTGGAGTTGTGGGGCGGTGGGAGGTCCTCAGAGGTGGGA
 GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCCCTCCCCCTCTCTGGG
 CACCCTCTGCCCCACACCATTTCCAGTGCAGGAGTCTGAGACCCCTTCCACCTCCCCACAA
 GTGCCCTCGGGTCTGTCTCCCCGTCTGGACCTCCAGCCACTATCCCTTGTGGAAGGCT
 CAGCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCTTGAAAACTTTAGGGTATTTTTGC
 GCAAACCTCCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAACCTTAAGCTGTTTTCT
 TAGCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTCTGCCCT
 CTAGCAGGAGGTTTTCCAACCTGTTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA
 CTGGGGGCTTCCGAGGCTCTCCCTCGACCTCTGTGCTCTGGGATGGCTGTGCGGAGCTGT
 ATCACTGGGTCTGTCCCCGGCTCTGTATCAGGCACCTTATAAAGCTGGGCCTCAGTGG
 GGTGTGTTTGTCTCTCTCTCTGAGCCTGGAAGGAAAGGGCTTTCAGGAGGAGGCTGTGA
 GGCTGGAGGACAGATGGAGGAGGCCAGCAGTAGCCATTGCACACTGGGGTGTATGGGTGG
 GGGCGTGACTGCCCCAGACTTGGTTTTGTAATGATTGTACAGGAATAAACACACCTACGC
 TCCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 34

MSSNKEQRSVAVFVILFALITILLYSSNSANEVFHYGSLRGRSRRPVLKKWSITDGYVPIL
 GNKTLPSRCHQCIVIVSSSSHLLGTLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
 SSVFVRLRRPQEFVNRTPTVFIFWGPSPKMQKPGSLVRVVIQRAGLVFPNMEAYAVSPGRM
 RQFDDLFRGETGKDREKSHSWLSTGWFTMVIARELCHVHVYGMVPPNYCSQRPRLQRMPYH
 YYEPKGPDECVTYIQNEHSRKGNNHRRFITEKRVFSSWAQLYGITFSHPST

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

FIGURE 36

MLRGTMTAWRGMREVTILACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEPP
 RMNVTVRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTIL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSTGNLQ
 IVNASQDEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARIYPPAEQTIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGGPGA
 AVILYNVQVFEPPEVTMELSOLVIPWGQSAKLTCCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQCAENEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTTPVSPSK
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEKGQGAPEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRTGRPRKPEIMASKEQQIQRDDPGASQSSSQPDHGRSLPPEAPDRPTISTASE
 TSVYVTWIPRGNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPSRLPYVVSQSGYGRVYERPVAGPYITFTDAVNETTIMLKWMIYPASNNNT
 PIHGFIYYRPTDSNDSDYKKDMVEGDKYWHSISHLQPETSYDIKMQCFNEGGESEFSNVM
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTMAMVARSSDLPLYLIVGVVLGSIVL
 IIVTFIPFLWRWASKQKHTTDLGFPKRSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRCPSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLNGYDPPQSHQITRGPK
 SSPDEGSFLYTLRDDSTHQLLQPHHDCCQRQEQPAAVQSGVRRAPDSPVLEAVWDPFPFHSG
 PPCCLGFLVPVEEVDSPDCQVSGGDWCPQHPVGAYVGQEPGMQLSPGFLVRVVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTGCTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC
CCAGGCTCCCGCGGCCGACCCCCGCGCAAC**ATG**CAGCCACGGGCGCGAGGGTTCCCGCGC
GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
CCGTAACCCGCGCGGAGACCAGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCCC
AGCCTCTTACCACGCGGGGTGTCCCCAGCGCCCTACTACCCAGGCCTACTACGCCAGG
CACCCCCAAAACCCTGGACCTTCGGGGTCGCGCGCAGGCCTGATGCGGAGTTTCCCACTCG
TGGACGGCCACAATGACCTGCCCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCTGGACAGGCTTAGAGACGGCCTCGT
GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCAGGACCAGACTGCCGTGCGCC
TCGCCCTGGAGCAGATTGACCTCATTACCCGCATGTGTGCCTCCTACTCTGAACCTCGAGCTT
GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
ACCTGACACTTACCTTACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTGAGACAC
CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCCTGG
AAGTGCTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG
TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAATATGACGGGACT
GGCCGGTTCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT
GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTTCGTGGAACCTGCTGCGGGTCT
TCAGACAAGTGGAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
CCATATGGGCACTGAGCACATCCTGCCACTCCCACTCGTGCCCTCAGAATGGACACCAGGC
TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCT
CCCCATACCTTGTTCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTC
TGCT**GGA**CACAGTCGGTCCCGCAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
AGTTCATTCACAAGCATATGCTGAGAATAAACATGTTACACATGGA AAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLRQPVTAEETPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVRSEESRAQSPVEAEFFYQGLSTSCH
SHLV PQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAG**CATG**
 AAGCTCTTATCTTTGGTGGCTGTGGTCCGGTGTGTTGCTGGTCCCCCAGCTGAAGCCAACAA
 GAGTTCTGAAGATATCCGGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
 TTTACAACCAGAAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
 GTGCTTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGTGCCTGTTGCTCT
 ACATGGCCTTCTCTGATGCTGGTGGACCTCTGATCCGAAAGCCGATGCATACACTGAGCAA
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAACACAGTCTTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC
 AAGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCT**TAGAT**GGGCTGG
 TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTCCTCCTT
 CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
 GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTTCGAGGCGGCTCAGGAGTGATGCGATCTGTCTCTCTGGCTCCACTCTTG
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCCTTGGAAAGATAAAGCTGGGTCTTCA
 GGAACCTCAGTGTCTGGGAGGAAAGCATGGCCCAGCATTAGCATGTGTTCTTTCTGCAGTG
 GTTCTTATCACCACCTCCCTCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCATGGA
 AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGGCCATGCATACT
 CTGCTGCCGGTCCCTCACCTGCACCTGAGGGGTCTGGGCAGTCCCTCCTCTCCCAGTGTG
 CACAGTCACTGAGCCAGACGGTTCGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCCTGTACTTGGGTTGCCTCTTGCTCCCTGAACCTCGTTGTACCACTGCATGGA
 GAGAAAATTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAAATTG
 TTTTATTCTCTCA

FIGURE 40

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGH DVEAYCLLCECRYEERSTTTIKVIIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEENEDARSMAAAAASLGGFRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

```

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCCTGAGGCGTGAGACTGAGTTCATAGGGCTCTGGGTCCCGGA
 ACCAGGAAGGGTTGAGGGAAACAAATCTGCAAGCCCCCGCGACCCAAGTGAGGGGCCCGGTGTTGGGGTCTCTCC
 TCCCTTTGCATTCCCAACCCCTCCGGGCTTTGCGTCTTCTCGGGGACCCCTCGCGGGGACGATGGGCCGCGTTGATG
 CGGAGCAAGGATTTCGTCCTGCTGCTCTCTACTGGCCGGCGGTGCTGATGGTGAGAGAGCTCACAGATCGGCAGT
 TCGCGGGCCAAATCACTTCATCAAGTCTCTCTGCGGCGGGGAGACGCGCTGGTCAGGCCCGCCACTCGATCTGCG
 GGCATGTACCAAGGACTGGCATTTCGCGCGGAGTAAAGAGGGGAAAAACCTGGGCGAGGCCCTACCCCTGTGACAGT
 GATTAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCTCGGCCTGCATGGTGTGTCGGAGA
 AAAAAAGAGCGCTGCCACCGAGATGGCATGTGCTGCCCGCAGTACCCTGCAATATATGGCATCTGTATCCCGATT
 ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCGGATGGTACTCGGCACAGAGATCGAAACCAACCGGTCTATTAC
 TCAACCATGACTTGGGATGGCAGAACTAGGAAGACCAACACACTAAGATGTACATATAAAGGGCATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGTTTGTGCTGTGCTCGTCATTCTGGACCAAAATCTGCAAA
 CCAGTGTCCATCAGGGGGAAGTCTGTACCAAAACACGCAAGAGGGTCTCATGGGCTGGAAATTTTCCAGCGT
 TCGCACTGTGCGAAGGGCTGTCTTGCAAAAGTATGGAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG
 TGTGAGAAATTTGATACCAATTTGAGGAACATCATCAATTCAGACTGTGAAGTTGTGTATTAAATGCATTATAG
 CATGGTGGAAAAATAAGTTTCAGATGCAGAAAGATGGCTAAAAATAAGAAACGTGATAAGAATATAGATGATCACAA
 AAGGGGAGAAAGAAACATGAATGAATAGATTAGATGGGTGACAAATGCAGTGCAGCCAGTGTTCCTATTATG
 CAACCTGTCTATGTAAATAATCTACACATTTGTGGAAAAATGCTATTATTAAGAGAACAGACACAGTGGAAAT
 ACTGTAGTGTAGCATGTGACTTTTCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCCTTCAGATTGCTGATTGT
 TATACAAATTAACCTACATGCCAGATTTCTATTCAAGCTTAGAGTTTAAACAAATCTCTTAGAATAACTTTGTA
 TACAATAGGTTCTAAAAATAAAATGCTTAACCAAGAAATGAAACATGGACAGTCTTGCTAGATAGAAGAAAAATCAGTCAAT
 TACCTTTTGATTGTGAACACTACTTCTGCTGTTCAATCAAGAGTCTTGCTAGATAGAAGCAATAAATAACAAACAAACAG
 TTCCAAATAATGCAAAATAATGGCCAGTTGTTTAGGAAGGCTTTTAGGAAGCAATAAATAACAAACAAACAG
 CCACAAATACTTTTTTTTCAAAATTTTAGTTTTACCTGTAAATTAATAAGAACTGTACCAAGCAAAACAGATGCTC
 TTCAGATTCTACGGAATGACAGTATATCTCTTTATCCCTATGTGATTCTGCTGTGAATGCATTATATTTTCCA
 AACTATACCCATAAATTTGACTAGTAAATACTTACACAGAGCAGAAATTTTCCAGATGGCAGAAAAATTTTAA
 GATGTCCTAATATATGTGGGAAAAAGGCTAACAGAGAGATCATTTATTTCTTAAAGATTGGCCATACCTATATTTT
 GATAGAATTAGATTGGTAATACATGTATTATACATACACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG
 CACTGGATGAAGCAAGAAAAATTTGGGAAACTTTTTCTGTTTGTACAGGTTTTGGCAACACATAGATCATATGTCTG
 AGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTGTCTAT
 CATAATATTACTATGCAGATGAATCAGTGTGAGGTCCTGTGCCGTACTATCCTCAAATATTATTTATTTATAG
 TGTCTGAGATCTCAATAATCTCAATTTAGGAGGTTTACAAAAATGTACTCCTGAAGTAGACAGAGTGTGAGG
 TTTCTAGTCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAACCTCTGCAGCATCTG
 CTTTATTGCCAAAGGCTAGTTTCGGTTTTCTGCAGCCATTCGGGTTAAAAAATATAAGTAGGATAACTTGTATAA
 AACTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATTTCTTGAACCACTTACTCTTTTTTAAACIT
 AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAAATAAAGGTTATCTTATAGTCTGTGACTTTTTTAAACIT
 TAGACCACAATTCATTTTCTTTATGTTTTCTTTTAAATCCCATCTGAGTCTCAAAATTAAGTTCCTCCAGTAG
 AGATTGAGTTTGAACCTGTATATCTATTAATAAATTTCAACTTCCACATATATTACTAAGATGATTAAAGACTTA
 CATTTTCTGCACAGGTTCTGCAAAAAACAAAAATATAAACTATAAACTCCAAGAACAAAGTTTGTATAAACAGGT
 TGTCTATAAGCTTTGAAATGAAATGGAACATTTCAATCAACATTTTCTATATAACAAATATTATATTACAAAT
 TTGGTTTCTGCAATATTTTTCTTTATGTCACCCCTTTAAAAATTTATTTTGAAGTAATTTTGAAGTACAGAAATG
 TTAATGAGATGTATTTCTTATAGAGATATTCTTACAGAAAGCTTTGTAGCAGATATATTTGCAGCTATTGAC
 TTTGTAATTTAGAAAAATGTATAAAGATAAAATCTATTAAATTTTCTCCTCTAAAAACTGAAAAAATAA
 AAAAAAATAAATAAATAA

FIGURE 42

MAALMRSKDSSCCLLLLLAAVLMVLESSQIGSSRAKLSIKSSLGGETPGQAANRSAGMYQGLA
 FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQGSSACMVCRRKKKRCRDMCCPSTRCNN
 GICIPVTESILTPHIPALDGTNRHRDRNHGHYSNHDLGWQNLGRPHTKMMSHIKGHEGDPCLRS
 SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
 SKARLHVCQKI

Signal peptide:

amino acids 1-25

2 kb
 1 kb
 500 bp
 250 bp
 100 bp
 50 bp
 25 bp
 10 bp
 5 bp
 2 kb
 1 kb
 500 bp
 250 bp
 100 bp
 50 bp
 25 bp
 10 bp
 5 bp

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAA
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGGCAACATCAGTTTTTAAAAATTGATT
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA
 TAGCTGCATTTATTTAGTCAGTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAAATCTTG
ATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAATGGCAAACA
 TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCTACAACCTACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCCCTCAGTCCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
 CAGTTCCTTAGCCAGTTGAGCCACGCACAACAGCACCAGAGCCAGGCAGTCACTGTTCTCTCT
 CCTGGTTTGGAGTCCTTTCTCTCCAGGCAAAACTTCGAGAATCAACACCTGGAGACAGTCC
 CTCACCTGTGAACAAGCTTTTGCAGCTTCCAGCAGCAGCATTGAAAAATATCTCTGTGTCTG
 TCCACCAGCCACAGCCCAACACATCAAACCTTGCTAAGCGCGGATACCCCAGCTTCTAAG
 ATCCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTACAGGATTAATATGTGCAGTT
 TGGGGCTCTGGAATTTGGGTGAGAACCCTTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTCCCATCAGCTTGTATTGCAAGTCTTTAAGTGAGCCTTTGAATACA
 TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGTCATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
 GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTTGTGCATGGCTGGTGCACCAACCAACAGAGGAAGGATAGCTCACGTGA
 TGTGGAACCAACAGTTGGTCAATGGCTCATTGCTTAAAGCAGCCCTTTTGCTTTTTTGT
 TTTTGACACAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTCAGCATACAGTATGCAT
 TTTAAAGATGCTTGGGCCAGCGGGGTGGCTGATGCCCATAAATCCCAGTGCTTTGGGGGGCC
 AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCTGGGCAACATGGTGAAACTG
 TGTCTCTACTAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCTGCCTGTAATCCAG
 CTACTTGGGAGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
 GTCTGAAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGE LAPPKMANITSSQILDQLKAPSLGQFTTT
 PSTQQNSTSHPTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSVLSQLSQRQQHQSQAVTVPP
 PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPQPKHIKLAKRRIPPASK
 IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT
 SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSESAP
 GTIMNGHGGGRSQQTLD SKYSSKLLLSWLVP TKQRKRIAHVMWKT PVGQWLIR

Signal peptide:

amino acids 1-24

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FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGCC**AT**GGCGCTGCCATCCCGAATCCTGCT
 TTGGAACCTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCGCGCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGGGGACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCGGG
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTGGGCGAGCGCCGCGCTA
 CGGGCCCCCTTTTCTGCGGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCTGCACGAACGCGCGTCTTCCACCTGACGGTGC CGGAACCCACGC
 GGAGCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGCGCCCCAGGCCACG
 ACCCCACACTGGCGCGCGGCCACAACGTCAATGTCATCGTCCCCGAGAGCCGAGCCAC
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC
 TGTCTCTGGCGCCCGCAGGCGCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGTTCCGGAAGGAGAACT
 GCAA**ATAG**GGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCCACCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAAAC
 AAAATCCCACTGATGCCCATCATGCCCTCAGACCCCTTCTGGGCTCTGCCCGCTGGGGGCTG
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAAGTGGGGTCAGCCTCA
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGCTGGGAGATGTTCTCGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT
 CCTCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTGCCCCATCCCTACCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCATCTGATTTTTAAAAA
 AAAAA

FIGURE 46

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQV VHWDRQPPGVPHDRADRLDL
YASGERRAYGFLFLDRVAVGADAFERGDFSLRIEPL EADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPPPRGSPGNGSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSP LPAKYIDLDKGFRKENCK

```

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGCGCGCTGGCGCAGCGGCGAC**ATG**GCCGTTGTCTCAGAGGACGACTTT
CAGCACAGTTCAAACCTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCT
GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTCTTT
ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCAGCCACCGGGGA
GGACCTTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCCTCCACCG
TGCCCTCCATGCTGTGCCCTGGTGGCCAACTTCTGCTTGTCAACAGGGTTGCAGTCCACATC
CGTGTCTGGCCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA
GGTGGACACTTCTCTCTGGACCCGTGGTTTTTTTTGGCGGTCAACATTGTCTGCATGGTGATCC
TCAGCGGTGCCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCCTATG
AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGACGGTCAGCGCCGTGGCCTC
ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG
CCACCATCTTCTCTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC
AGGTACTACATGAGGCCTGTTCTTGGCGCCCATGTGTTTTCTGGTGAAGAGGAGTTCCCA
GGACTCCCTCAGTGCCCTTCCGTTGGCTCCAGATTCAATTGATCCCAACACCCCTCTCC
GCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTCACTACGTCTTCTTCATCACC
AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCTGTACAACTTTGCTGACCTAT
GTGGCGGCGAGCTCACCAGCTGGATCCAGGTGCCAGGCCCAACAGCAAGGCGCTCCAGGG
TTCGTGCTCCTCCGGACCTGCCCTCATCCCCCTCTTCTGTGCTGTAACTACCAGCCCCGCT
CCACTTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCGCACTCCTCAGCTCCCTGCTGG
GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTCAGGGCCTAAGATTGTGCTCCAGG
GAGCTGGCTGAGGCCACGGGAGTGGTGTATGTCCTTTTATGTGTGCTTGGGCTTAACACTGGG
CTCAGCCTGCTCTACCTCCTGGTGCACCTCATC**TAG**AAGGGAGGACACAAGGACATTGGTG
CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCC
TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA
GTGAGCCACGTCATGCCATTCCGTCAGGCGAGATATTCCAGTCAATTAACAGAACACT
CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACAGCTGATGGTTA
ACATTCCACCTTCTTTTAGCCCTTCAAAGATGCTGCCAGTGTTCGCCCTAGAGTTATTACA
AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCAGCTGCGCTCATTCAGCT
GACAGCGAGATGCAAGCAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA
AGTCCCCCTGGCATGGTCAGTCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
CGGGGTGAACAACTGCCCACTAACCAGACTGGAAAAACCCAGAAAGATGGGCCCTTCCATGAAT
GCTTCATTCCAGAGAGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
TTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCTGGGTCAAGATGAGGGT
TTTCAGTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC
GTATTCAAAA

FIGURE 48

MAVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLRPEDRFCGTYYIFFSLGI
 GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSILNYFESYLAVASTVPSMLCLVANFL
 LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
 YGMTGSFFMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
 LLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF
 CVTYVFFITS LIYPAVCTNIESLNKSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
 GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
 305-330, 448-472

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FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTGCTGTACCAAGAGCTGGAGACACCA
 TCTCCACCGAGAGTCAATGGCCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCTCTCC
 TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGGCCAAGACCCCTTCGAGAAATGC
 ATGCAGGATCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCCT
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGCCCGGGCTGGTGGCCGCCAAGGTGC
 TCAGCGATGCTGGACACAAGGTCACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGGCTCAACCTGACCAAGTTCACCC
 AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
 AAGGTGCCCGAGAAGCTGGGCTACGCCTTGCGTCCCCAGGAAAAGGGCCACTCGCCCCAAGA
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG
 CGATGAAGAAGTTTGAAGGCACACGCTCTTGAATATCTTCTCGGGGAGGGGAACCTGAGC
 CGGCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT
 CGCCGAGGCCCTCCGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG
 GTGGCTGGGACCTGCTGCCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC
 GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCGAGATCGAGACCTCTCC
 CCCGGCGCGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG
 CGGTGAAGCGCATCACCTTCTCGCCGCCGCTGCCCCGCCACATGCAGGAGGCGCTGCGGAGG
 CTGCACTACGTGCCGGCCACCAAGGTGTTCTTAAGCTTCCGAGGCCCTTCTGGCGCGAGGA
 GCACATTGAAGCGGCCACTCAAACACCGATCGCCGTCGCGCATGATTTTCTACCCGCCGC
 CGCGCAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTGGACGCGGCGGCAGCGTTCGCC
 GGC TTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC
 TGTGCTGCCAGCTCTGGGACGGCACCGCGTCTGTCAAGCGTTGGGCGGAGGACCAGACAA
 GCCAGGTTGGCTTTGTGGTACAGCCGCCGGCGCTCTGGCAAACCGAAAAGGATGACTGGACG
 GTCCCTTATGGCCGCATCTACTTTGCGGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA
 GACGGCGGTCAAGTCGGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCTGCAT
 CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG
 GTGGCCAGCAGCCCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCCTCCAGTCCAAGG
 CCAGTTATCTCTCCAAAACAGACCACACGAGGACCTCGCATTAAAGTATTTTCGAAAAA
 AA

FIGURE 50

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTVWGLNRTLKPQRV
 IVVGAGVAGLVAAKVLS DAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPS SHRIL
 HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPKLG YALRPQEKGHSPEDIYQMA
 LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMS EDGFFYLSFAEALR
 AHSCLS DRLQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGP HDVHVQIETSPPARNL
 KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRR LHYPATKVFLSFRPFWREEHIEGG
 HSNTDRPSRMIFYPPREGALLASYTWS DAAAAFAGLSREEALRLALDDVAALHG PVVRQL
 WDGTVVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
 ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHG VASSPSHDLAKEEGSHPPVQQLSLQ
 NTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAAGCTGGGGACACTCTGGGCGGCCCTCTGCGCTGCAT
GGACGCTCTGAAGCCACCTGTCTCTGGAGGAACACGAGCGAGGGAAGAAGGACAGGGACTCTGCTGTGGCAGGAA
 GAACCTCAGAGCCGGGAAGCCCCATTCACTAGAAGCACTGAGAGATGGGCGCCCTCGCAGGGGTCTGAATTTCT
 GCTGCTGTTTCAAAAGATGCTTTTATCTTTAACTTTTTGTTTTCCCACTCTCCGACCCCGGGGTGATCTGCAT
 CTTGACATTTGGAGCTGCCATCTCTTTGTGGCTGATCACCAGACCTCAACCCCTCTTACCTCTCTTTGACCTGAA
 CAATCAGTCTGTGGGAATTTAGGGAGGAGCAGCGAAGGGGGTTTCCCAGGAAGACATGACCTAACAAGTTGCTG
 CTTCTCAGATGCCAAGCATATGATATAGGTTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCTCTGTGGG
 ATATAGAAAACCAACAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTATAGAGCAGAGTACCTGGGTTG
 CTGTCTCTTGTCAATAAGGTTATAAATCATCACCAGACCACTTTGTCCGATCTTTGCTCAGAATGAGCCAGAGTC
 GATCATCTCCGAATTTGGCTTTGTACAGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACAGAGAAGC
 CATCGTACATATTTGCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCAAAAGGCATTGGTGCTGAT
 AGGGAATGTAGAGAAGGCTTCAACCCGAGCCTGAAGTGATCATCTTATGGAACCCCTTTGATGATGACCTGAA
 CAAAAGAGGGGAGAAGATGGAATTTGAGATCTTATCCCTATATGATGCTGAGAACCCTAGGCCAAAAGACACTT
 CAGAAAACCTGTGCCCTCTAGCCCAAGAAGACTGAGCGTCAATCTGCTTACCAGTGGGACCACAGGTGACCCCAAAGG
 AGCCATGATAACCATCAAAATATTTGTTCAAATGCTGCTGCCCTTCTCAAATGTGGAGCATCTTATGAGCC
 CACTCTGATGATGTGCCATATCTACCTCCCTCTGGCTCATATGTTTGAAGAGATGTACAGGCTGTTTGTTGA
 CAGCTGTGGAGCCAGAGTTGGATTTCTTCAAAGGGATATTCGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
 CACATTTGTTCCCGCGGTGCCCTCGACTCTTAAACAGGATCTACGATAAGGTACAAAATGAGCCCAAGACACCCCT
 GAAGAAGTCTTGTGTGAAGCTGGCTGTTTCCAGTAATTTCAAAGAGCTTCAAAGGGTATCATCAGGCATGTATAG
 TTTCTGGGACAAGCTCATCTTTGCAAAAGATCCAGGACAGCTGGGCGGAAGGTTGCTGTAAATTTGCTACTGGAGC
 TGGCCCCATGTCCACTTCAGTCATGACATCTTCCGGGCGAGCAATGGGATGTGAGTGTGTGAAGCTTATGTGTCA
 AACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGGACTGGACATCAGGTCACTGTGGGTTGCCCTGSC
 TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTTTACAGTGAATAAAGAAGGAGAGTCTGCAT
 CAAGGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCTGAGAAGACACAGGAAGCCCTGGACAGTGTATGGCTG
 GCTTCACACAGGAGACATTTGGTCGTGGCTCCCGAATGGAACCTCTGAAGATCATCGACCGTAAAAAGAACATTTT
 CAAGCTGGCCCAAGAGAGAATACATTTGCAACGAGAGAAGATAGAAAATATCTACACAGGAGTCAACCAAGTTTACA
 AATTTTTGTACACGGGAGAGCTTACCGTATCCCTTAGTAGGAGTGGTGGTTCTGACACAGATGTACTTCCCTC
 ATTTGACGCCAAGCTTGGGGTGAAGGGCTCCTTTGAGGAATGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTT
 AGAAGACTTCGAGAAAATTTGGGAAGAAAGTGGCCTTAAACACTTTTGAACAGGTCAAAGCCATTTTCTTTATCC
 AGAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTTGAAAGCAAAGCGAGGAGAGCTTTCCAAATACT
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAAGATAAGGTACTTAAGTACTCGCCGGCCCACT
 TGCATGCTGTGTGAGAAAATGGATTAAAAAATATTCTTACATTTGTTTTGCCTTTCCCTCATTTTTTTTTTAAAC
 TGTTAAACTCTAAAGCCATAGCTTTTGTTTTATATTAGACATATAATGTGTAAACTTAGTTCCCAATAAATCA
 ATCTCTCTTTCCCATTTTGCATTTTGTCTATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA
 GATCCAGTTTATGTCTGTGTCCTTCTCATGATTTCCAACTTAATACTATTAGTAACCAAGTTCAGGGT
 CAAAGGGACCCCTCTGTGCTTCTTCTTTGTTGATAAACATAACTTGCCAAACATCTCTATGCTTTATTACA
 TCTTCTACTGTTCAAACCTAAGAGATTTTTAAATCTGAAAAAAGCTGCTACAAATCATGTTTCTAGCCACTCCAC
 AAACCACTAAATTTTAACTTTTGGCTTATGACCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT
 CTGCGTAAATTAATTTGTACTGAAGGAAAAGTTTGATCATACCAAACTTCTCAAACTCTCTAGTTAGATA
 TCTGATCTGGGAGTATTAATAATTTGGGCTATGACATACCTGTCAAAAGGAATGCTGTTCTTTAAAGCATTTATTA
 CAGTAGGAACCTGGGAGTAAATCTGTTCCTACAGTTTGTCTGAGCTGGAAGCTGTGGGGAAGGAGTGACA
 GTGGGCGCCAGTGACTTTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACCTCTGAACCTGGGAACAAGATCT
 ACAGGCAAGCAAGATGCCACACACAGGCTTATTTCTGTGAAGGAACCACTGTACTCTCCCCACCCCTTGATT
 AGAGTCTGCTCTACCTTACCACAGATAACACATGTTGTTCTACTTGTAAATGTAAGTCTTTAAATAAAC
 TATTACAGATAAAAA

FIGURE 52

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775

<subunit 1 of 1, 739 aa, 1 stop

<MW: 82263, pI: 7.55, NX(S/T): 3

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLFTKMLFIFN
 FLFSPLPTALICILTFGAAILFLWLITRPQVPLLLDLNNQSVGIEGGARKGVSQKNNDLTS
 CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYQVSDRAEYLGSCLLHKGYKSS
 PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPFAIVHIVNKADIAMVICDTPQKAL
 VLIGNVEKGFTPSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
 LSVICFTSGTTGDPKGAMITHQNIIVSNAAFLKCVHAYEPTDDVAISYPLAHMFERIVQ
 AVVYSCGARVGGFFQGDIRLLADDMTLKTPLFAVPRLNRIYDKVQNEAKTPLKKFLLKLA
 VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGRVRVIVTGAAPMSTSVMTFFRAAMGCQVY
 EAYGQTECTGGCTFTLPDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
 GYLKDPEKTQEALDSGWLHTGDIGRWLPNGTLKIIDRKKNI FKLAQGEYIAPEKIENIYNR
 SQPVLQIFVHGESLRSSLVGVVVPDPTDVLPSFAAKLGVKGSFEELCQNQVVRFAILEDLQKI
 GKESGLKTPEQVKAI FLHPEPFSSIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGCGGAGGCCGCGGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG
 CCCGGGGCCCTAAGCCATTCTGTAAAGTCATGGGCTGGCCAGGACATTTGGTGACCCGCCAAT
 CCGGT**TATG**GACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
 GACAGGGGGCCGTGCTTTTCTGCTGGTGACTGTCAATGTCAATATCAAGTTGATCCTTGGACA
 CTCGGCGAGCCATCACTGGAAGCCAAATGAAGACCAGAGCCAGAGCCAAGACTATGATGAGGCC
 CTAGGCGCCCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG
 AGGCCCGGGAGCAGGGCCGGGGCATCCATGTCTTGTCTCAACCAGGCCACGGGCCACGTG
 ATGGCAAAACGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTCT
 CAACATGGTAGCGCCCGGCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC
 TGGAGGGACACATGGGCCTTCGTGGGACGAAAGGAGGTCTGTCTTCGGGGAGAAACATTC
 TAAGTCACCTGCCCTCTCTTCTGGGGGACCCAGTCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCCGCGGGCGC
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGATGCAGCTGCAAGGACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCAGACAACAAGGTCTCTCAATGTGCCTGTGGCTGTCAATGAGC
 GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCAGGGGGTGTCT
 CCTCAGATGATAACAGTTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAAATGCCCGCTGTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGTGTGGTT
 CTGGAAGAGGACCTGGACATGTCTGTGATTTTTTCAGTTTCTGAGCCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA
 CGGCTGAGGACCCAGCCTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC
 AGGAGGTCTTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGATCATCCTGACG
 TTTCCGATCTCCACTTTTGCCATCGTCGGCCTCAACATGAATGGCTACTTTACAGAGGCC
 TACTTCAAGAAGCACAAAGTTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT
 GAAGAAGAAGCTTATGAAGTGGAAGTTCAACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
 ACAGCAAGAACCCTTGTGAAGACTCTTTCTGCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTATTCGAATGGAGAAAGATGATGACTTCAACACCTTGGACCCAGCTTGCCAAGTGCTCCA
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCCCTGTGGAGATTGTTTCGGAAGAAGA
 ACCACTTCTGTGGTGGGGGTCCCGGCTTCCCTCTACTCAGTGAAGAAGCCACCCCTCAGTC
 ACCCCAATTTCTCTGGAGCCACCCCAAGGAGGAGGGAGCCCAAGGAGCCCAAGACAGACAG
ATGAGACCTTCCCTCAGGACCTCGCGGGCTGGGTACTGTGTACCCAGGCTGGCTAGCCCT
 TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTTAACA
 TGAGACTTAAATTACTAACTCAAGGGGAGGGTTCCCTGCTCCAACACCCCGTTCTGTAGTT
 AAAAGTCTATTTTATTCTTCTTCTTGTGGAGAGGGCAGGAGATACCTGGGAATCATACG
 ATCCCTAGCAGCTCATCTGCCCTTTGAATACCTCACTTTCCAGGCCTGGCTCAGAACTTA
 ACCTATTTTATTGACTGTCTGAGGGCCTTGAAAAACAGGCCGAACCTGGAGGGCCTGGATTTC
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTTACTCAGGAACCTGCTGTGCC
 CAACCCATGGACAGGCCACGTGGGGCCACATGCTGACACAGACTCAGCTCAGAGACCCCTTA
 GACACTGGACCAAGGCCTCTCTCAGCCTTCTCTTTGTCCAGATTCCAAGCTGGATTGAATT
 GGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 54

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVPDITYSPHEDEAMVLFNLNVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSAQAPALGWRDTPWAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRNRRRRCFCVVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLRLRLSLLSAQGVSPQMITVFIDGYEEFMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFAVLEEDLDIAVDFFSFLSQSIHLEEDDSLICYISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKKHENTVPGVQLRNVDLSLKKEAYEVEVHRLLEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDFTTWTQLAKCLHIWDLVDVRGNHRGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKKEGAPGAPEQT
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Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACAC
 CTGTTTAAAGAACCTAAGCACCATTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA
 AAGGAGGGCAGAA**ATGGAT**GATTTCATCTCCATTAGCCTGCTGTCTCGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTGG
 GTGCTGGCCTTCTCTGTGGAACCTGCTCTGGCAGTCATCGTGCTGAAGGAGTACATGCCCTTTATGAA
 GATATTCTTGAGGGAAAACACCCAGCAAGTGAACACATAATGTGATTGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACACAGCTCATGCGCTATATTGGTG
 TTTCCCTCGTTCTGGGCTTGGTTTTCATGTTGCTGGTGGACAGATTGGTAECTCCATGTGCATTCT
 ACTGACGATCCAGAAAGCAGCAAGCTCTAGCAATTCCAANAATCACCACCACGCTGGGTCTGGTTGTCCA
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG
 TGTTTGTGGCAATCATGCTACATAAGGCACCAAGCTGCTTTTGGACTGGTTTCTCTTGTGATGCATGCT
 GGCTTAGAGCCGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTTCTCTGCCGGGACATTTCTTATGTTGCCACAGTACATGTCCCTCCCTGAGGTGGGCGGA
 ATAGGGCACGCCACAAGCCGATGCCACGGGAGGGAGCGCTCAGCCGCTCGGAAGTGGCAGCCCT
 GGTTCCTGGGTGCTCATCCCTCTCATCTCTGTGCTAGTAGGACACAGCAT**TAA**ATGTTCAAGGTCAGC
 CTGGTGCAGGGCCGTTTGGCATCCAGTGAGAACAGCCGGCAGCTGACAGCTACTCATCTCTCTCAGTC
 TCTTGCTCACCCTTGGCAGCTCTCATAGTATTCTTAGAGTCCAGAGGGGAGGTGAGGTTTAAACCCTG
 AGTAATGGAAAAGCTTTTAGAGTAGAAAAACATTTACGTTGCACTAGCTATAGACATCCCATTTGTGT
 TATCTTTTAAAGGCCCTTGACATTTTGCCTTTTAATATTCTCTTAACCCATTTCTCAGCGGAAGATG
 GAATTTAGTTTAAAGGAAAAGGAGGAACCTCATACTCACAATGAAATAGTGATTATGAAAATACAGT
 GTTCTGTAATTAAAGCTATGCTCTTTCTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATGATTTTTT
 AACATGSGTCCCACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTCATA
 GCACCCACTCACTTAGATGCTAAAGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAAATGATAGC
 AAGACACATTGAAAGCTCTCTTTATACTCAAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATT
 TAAACAGCTCCTTTGGCAGCTGCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTGTAGCATTCCTTGTCAAGTTCTCCTTTGCAGAAT
 ACCTGTCTCCACATCTCTAGAGGAGGCCAAGTTCTAGTAGTTTCAAGTTCTAGGCTTTCCTTCAAGAA
 CAGTCAGATCAAAAGTGCTTTTGGAAATTAAGGGATATTAATTTTAAAGTATTTTGGATGGTTAT
 TGATATCTTTGTAGTAGCTTTTTTTAAAGACTACCAAAATGATGGTTGTCCTTTTTTTTGTTTTTT
 TTTTTTTTAAATATTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTCAGCTTT
 GGGCAGACTGTGCTTCTCACAATAACCACCTGTAGCAAGATGGATCAATAATGAGAAGTGTTTGCCATA
 TTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCGCTCTTTTCTTGGCTTTTCTCTTAACCTT
 TCCCTCTAGGCTCTCCTGCCCAAAATTTGCTGCTTACTGCTGGTGTAAATATTGTGTGGGATGAATT
 CTTATCAGGACAACCACTTCTCGAAGCTAATAATGAAGATAATAATATCTTTATTCTTTATCCCTT
 CAAAGAAATTAACCTTTGTGTCAAAATGCCGCTTTGTGAGCCCTTAAATACCACTCCCTCATGTGTAA
 ATTGACACAATCATAATCTGGTAATTTAAACAATTTAGATAGCAAAAGTGTTTAAACAGACTAGGATA
 ATTTTTTTTTCATATTGCCAAAATTTTGTAAACCCCTGTCTTGTCAAAATAGGTGTATAATATTGTAT
 TATTAAATTTATTTTACTTTTCTATACCATTTCAAACACATTACACTAAGGGGGGAACCAAGACTAGTT
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAACCGTTTCTATGACGCATAGCTAGCATGCCTATG
 ATTTATTCTCTCATGAATTTGTCTAGTATCAGCAGCTGTGGAATAAAGCTTGTGAGCCCTGTCT
 GGCCACAGTGAGGAAAGTAGCACAATAGGATACAGTTGTATGTAGTCATTGGCAACAATTGCATACA
 ATTTTACTACCAAGACAAGTATAGTATGGAAGTCCAAATGACTTCCTGTGATTGGATGTTAACAGCT
 GACTGCTGTGAGACTTGAGGTTTCATCTAGTCCCTCAAACATATAGTTGGCTAGATTCTCTCGGA
 AACTGACTTTGTCAATAAATAGCAGATTGTAGTGTCAAAAAA

FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
 YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMILLVDQ
 IGNSHVHSTDDPEAARSSNSKITTTTLGLVVHAAADGVALGAAASTSQTSLVQLIVFVAIMLHK
 APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
 FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILLSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

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FIGURE 57

GCTCGAGGCCGCGCGCGCGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC
 CGAGTGGCGGCCGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGACATGATGGGCTTGG
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGCAGGCGGGCTGCAGAGAGAGGCGCGCTGGAGCTGAAGA
 AGAACGAGTTCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA
 TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
 AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTCAACAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCTTGCCACACACAGAGGTGCCACAAGGAAGGGAACGTGCTTGGTAACAGCAA
 GTCCCAGACACCAGCCCCAGTTCGGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAAG
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
 CCAGGCCGGGAGCAGGTGGTGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCACTGAGCCAGGAAAATCCAGAGA
 TGGAGGGCCCTGAGCGAGACCAGCTTGTATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT
 GCCGGGGAAGGAGAAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
 TTTTAAATGTTGAAGATCAGAAAAGAGACACCATAAAATTTACTTGATCAGCGTGAAAAGCGG
 AATCATACACTCTGAATTGAACTGGAATCACATATTTACAACAGGGCCGAAGAGATGACTA
 TAAATGTTTCATGAGGGACTGAATACTGAAAAGTGTAAATGTACTAAATAAATGTACATCTGA

FIGURE 59

GGATGCAGAAAGCCTCAGTGTGCTCTTCTGGCCTGGGTCTGCTTCTCTTCTACGCTGGCATTGCCCTCTTCA
 CCAGTGGCTTCTGCTCACCCTGTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCG
 TGCCATTGGGGGAGCCAGGGAAACCTGGGGCTGCTGGATGGCTTCCGATTTTCGCGGGTTGTGTTGGTGCTGA
 TAGATTGCTCTGCGATTTGACTTCGCGCAGCCCCAGCATTACACGCTGCCATGAGAGGCTCCTGTCTCCCTACCTCT
 TCTCGGGAAACTAAGCTCCTTGCAAGGATCCTGGAGATTACGCCCCACCATGCCCGCTCTACCGCTCTCAGG
 TTGACCTCTTACCAACCCATCAGCGCCTCAAGGCCCTCACCATTGGCTACTGCTACCTTTATTGATGCTG
 GTAGTAATCTTGCAGCCACGCCATAGTGGAAACAATCTCATTAGCAGCTCACCAGTCAGGAAGGCCGTGTAG
 TCTTCTATGGGAGATGATACCTGGAAAGACCTTTCCCTGGTGCTTTCTCCAAAGCTTTCTTCTTCCACTCTCA
 ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAAACCTCTACCCACCATGGACAGTGGTGAATTGGG
 ACGTGTGATTGCTCACTTCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCTGAAATGGCCA
 AGAACTTAGCCAGATGGACCAAGTGATCCAGGACTTGTGGAGCTTGAGAGATGACACACTGCTGGTAGTGG
 CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAAGTGGAGTCTCAGCTGCTCTCTTTC
 TGTATAGCCCCACAGCAGTCTTCCCGACACCCACAGAGGAGCCAGAGGTGATTCCTCAAGTAGCCTTGTGCG
 CCACGCTGGCCCTGCTGCTGGCCCTGCCCATCCCAATTTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG
 GGGTGAGGACTCCAGCCCCACTCCTCTGCTTTAGCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
 CCGGATTTCTTCACTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTGT
 TCTCCAAGCCTCTGCTGACTCAGTGGCTTCTCCAGAGCCCAAGGGGGCTGAGGCGACACTGCCGACTGTGA
 TTGCTGAGCTGCAGCAGTTCTCGGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTGC
 CGATGCGGGGGGTACTGCTCTTGGCTGCTTCTGCTTTATCTGCTGCTGGCATCTCAGTGGGCAATATCCC
 CAGSCTTTCCATTTCGCCCTCTACTCTGACACCTGTGGCCTGGGGCTGGTGGGGCCATAGCGTATGCTGGAC
 TCTCGGGAATATTGAGCTGAAGCTAGATCTAGTGCTTTAGGGGCTGTGGCTGCACTGAGCTCATTCCTCCCTT
 TCTGTGGAAAGCCTGGGCTGGCTGGCCGCTCAAGAGGCCCTGGCAACCTGTTTCCATCCTTGGGCCCTGCC
 TGTACTCTGCTGTTTGGCTTGGCTGTGTTCTCTGATAGTTTGTGTTAGCTGAGGCCAGGGCCACCCCT
 TCTTCTTGGGCTATTATCCTGCTCCTGTTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC
 TCACATGCCCCGCTTGGCACTTCAGCCACAACACCCCCACGGGACAAATGGTGATATGCCCTGAGGGTTG
 GAATTGGGTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTGGCACT
 CCTCTCCTGCTGAGTCTCTGGCATCCATGGTGGTGGTGCAGCCAGAATTTATGATGAGAGCTTGTGTGG
 CGCGCTGTGGCCCTGTAGCTGCCGTGCGCTTGTGGCTCGCCGCTATGGTAATCTCAAGAGCCCCAGGCCAC
 CCATGCTCTTTGTGCTGGGAGTGCCTAATGGCAATGGGTACTGCTGCCACTGGGCATTGGCGTCCGGGG
 CAGATGAGGCTCCCCCGCTCTCCGGGTCTGGTCTCGGGGCATCCATGGTGCTGCCCTGGGCTGTAGCAGGGC
 TGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGTTGAGGCTGGGGCAGGCGCTCCAA
 GGACCAGCACTGCTCCTCACTCCCTTCTCAGGCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAA
 TCTACCGACACATCAGGAGGAGTTCGGGGCCGGTTAGAGAGGACCAATCTCAGGGTCCCTGACTGTGGCTG
 CTTATCAGTTGGGAGGTCTACTCAGCTGCTATGGTCACAGCCCTCACCTGTTGGCTTCCCATTCTGCTGT
 TGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTTTCTGAGAGCTTCCCTTCCATACATCTGCTGTGCTG
 CTGGGATACCGCTCACCACCTCTGCTCTTTACTGTGCCATGGCAGGCACTCGGCTTGGGCCCTCATGGCCA
 CACAGACCTTCTACTCCACAGGCCACAGCCTGTCTTCCAGGCATCCATGGCATCAGGCTTCTCGGGATTTCC
 CAGAGGCTCATGGCTGCTGACTTGGCTGCTGCTTGTAGTGGAGGACCAACCTTGGCTCCGCTCCTCTCT
 TTGCACTAGTTGCCACTGCTCTGCTGTGGCTTTCTGTGTGAGAGTCAAGGGCTCGGGAGAGACAGCAGC
 CCCCAGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGTGAGAGATCGCGCTCCGG
 ATGCGCTCAGCATTCTATGACGACTGCTGCAGCTGGGCCCTCAAGTACCTCTTTATCTTGGTATTCAAGTAT
 TGGCCTGTGCTTGGCAGCCTCATCTTGCAGACCTCATGTGCTGGAAAGTGTGGCCCTCAAGTTTCAAT
 TTGAGCTGTGGCTTCATTGTGAGCAGCTGGGACTTCTCTGGGCATAGCTTTGGTGATGAGATGGATGGTG
 CTGTGAGTCTGCTGTTTCAAGCAGTATTCTTGGCCACAGAGCTAGCTAGTCTGATTACTGGCATTTGGCT
 ACGAGAGTGCTGGAGAACCTGTAGCCTGGCCTGTACAGTACTGGATGATCTGCAGACAGGCTCAGCCATAC
 TCTTACTATCATCGACGACGGGGCCGCTGACATCTAGACCTTCAATATTCTAATTCAGGACCAAGTGGAGTA
 TGATCCTTACTCTGACTTATTTGGATGCTCTGAGGGAACAGGGGGCGGTCTCCGAAGTGGAAATAAATGAGCCG
 CGGTGGTACTTCCACTTAATCCAGCACTTGGGAGCAGAGGTGGGAGGATGCTTGGTCCCGAGGATGCTCA
 AGACCAGCCTGTGGAACATAACAGACCCGCTCTACTATTAAAAAAGTGTAAATAAATGATAATAT

FIGURE 60

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLEYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGKPGACW
MASRFSRVVLVLIDALRFDFAPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTTMQRKLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF
PGAFSKAFFFPSENVRLDITVDNGILEHLYPTMDSGEWDVLIHFLGVGDHCGHKHGPHPPEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTTNGDHGGDSELEVSAALFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLLGLPIPFNGIGEVMAEFSGGSDSQPHSSALAQASALHLNAQ
QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAIISPGFFPCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFRILA
VFFSDSFVAEARATPFLGGSFILLVVLQHWEGQLLPKLLTMPRLGTSATTNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALIA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPRLRLVLSGASMLVP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTFFSGPPTSQADLDYVVPQIYRHMQE
EFRGRRLERTKSQGPLTVAAYQLGSVSYAAMVTALTLLAFPLLLLHAERISLVFLLLFQSF
LLHLLAAGIPVTPGPFVTPVQAVSAWALMATQTFTYSTGHQPVFPAIHWHAAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLLCESQGLRKRQPPGNEADARVRPEEEEEP
LMEMLRLDAPQHFYAALLQLGLKYLFIILGIQILACALAASILRRRLMVVKVFAPKFTFEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGT
 GTCTCTGGTGGTTTGCCATAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**ATGT**
 CCTACAATGGACTCCACCAGAGGGTCTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT
 CCTGACAGCTCCAGAGAAGTGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA
 TATATCCAACTCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT
 ACACGTGGAGTCCTTCGTCGCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTG
 CCCATATCTATTACCGTGTCTTTCTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAATGAATTTGACAAA
 GATTCTTTGTGCTGTGTGA**AAAAA**ATCGTGATTAACCTTTATCACCCCTCAATATCTCGGATGAT
 TCTAAATTTCTCATCAGGATATGAGTTTACTGGG**AAAAA**AGCAGTGATGTATCCAGCCTTAA
 TGATCCTCAGCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
 GGTATGCTTCGCATTTGATGGAAATTTTTGTGACTCTGAAGAAACACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAAATACCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCACTGACATTTGTGCGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGAGGCAGCGTTGGCAGTCTTGGGCCCG
 CAAACGTTACAGTACTATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCCCTGGTCGACTGGGATCCCC
 AAAC**TGGCAGGCTGTGTATTCTTCGCTGT**ECAGCTTCGACCAGGATTCAGAGGGCTGCGAG
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCTATGGAGGAATGGGGT
 TATATGTGCAGATGGAA**AACTGA**TGCCAACACTTCCTTTTGCCTTTTGTTTCTGTGCAAC
 AAGTGAGTCACCCCTTGATCCAGCCATAAAGTACCTGGGATGAAAGAGTTTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTCTCTATTCTCATAGCACGTGTGTGATTG
 GTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT
 GTTCTATGCAGAGAAAGCAGTCAATAAATGTTGCCAGACTGGGTGCAGAATTTATTCAGG
 TGGGTGT

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSSISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
 QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
 CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIYHVGKEKHPANLILYGNFED
 KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSSLNDPQPSGNLRPPQEEEEVKH
 LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYEDVRTTDICAGPEEQELSL
 QEEVSTQGTLLSQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD
 PQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEEGLLSRLYEAPDRPPGENETYLMQFMEEW
 GLYVQMEN

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGGCCAAATCACTGCGGA
GGCTTCTGCTGCGAGCCCGCTGGGTGGTCTCGGCGGCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGTGTTGGCGCCACGTCTGAGTACTGCGGAGGCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACCACGACCCCGACTACCACCCCATGACCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGACG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCC
CCAGCCCGGCCCTGCCTGGGACCACCAGGCCCCAGGAGAAGCCGCC**TGAG**CCACAACCT
TGCGGCATGCAAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTCAAGGTTGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAATGTTAACTGACAAAAAAAAAAAAAAAAAAGAAA

FIGURE 64

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSAEPTQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTLMCTRSRGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLEGTTRPPGEAA

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Signal peptide:

amino acids 1-30

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FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA
 CGCCTGTCCCCGGCCCGGCATGAGCCGCTACCTGCTGCCGCTGTCCGCGCTGGGCACGGTAG
 CAGGCGCCGCGCTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC
 ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
 GGAAGTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGCGGGAGACCCCTCAATCACCATGTCAACGCCCGGCACCTGGAC
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGCAAAGATCATTGAAGAGGAGGAGCGAGT
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT
 TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
 GCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG
 CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA
 GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT
 TCCGGAAGTACTTCGATGGACTCAACAGAAGGCCCGGCCCGGAGGCTGAGGATGAGGA
 GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA
 GGGAGCAGCCCCCTCCCGAGATTAACTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG
 ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTTGGCACTACCTGAGCCGGGAGACCCAG
 GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGACTGGC
 CTGCAAGTGAGCACTGCCCGGGCTCTGGCTGGTTCGCTCTGCTCTGCTGCCAGCAGGGGAG
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
 TGTGCACTTGACAGCCACGTGAGGAGAGCCAGCGGTGCCGTGCGGGAGGGTTCCAAGGTGC
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT
 TGTGCATGCATGGTCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTG
 CTGTCTCCCATGATGGTGTGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
 GGTGTTTGCTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC
 GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGTACAGGACCTGGGA
 TTGCTGGGACTCCCACCTTCTCATTAATCTCATGGTAGTCCAACTGCAGACTCTCAAA
 TTGCTCATTT

FIGURE 66

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHGLGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPiFWLLVKSPELAAQPSSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

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Signal peptide:

amino acids 1-17

/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
 ><subunit 1 of 1, 331 aa, 1 stop
 ><MW: 35932, pI: 8.45, NX(S/T): 1
 MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
 GNIILACRDMEKCEAAAKDIRGETLNHHVNNARHLDLASLKSIREFAAKIIEEEERVDILINN
 AGVMRCPHWTTEDGFEMQFGVNHGLGHFLLTNLLLDKLKASAPSRIINLSSLAHVAGHIDFDD
 LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
 SSTTLGPiFWLLVKSPELAAQPSSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
 AESARLVGLEAPSVREQPLPR

FIGURE 67

GAAGTTTCGCGAGCGCTGGC**ATGT**GGTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
 GCCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACAGTTCTCGGCGCTGAC
 CAGCGTGGCGCGCGCCCTGGCGCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT
 GAGGATTCAACAACCCCTGTGGCTAACCCCTGCTGCTTGCATTTACTCTCATCAAACGCCCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCCTTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCTGATGCGGCTGCAGGACCTGTACATGCTCAATGTGAAAGGCCCTGGCCCGAGGTGTCTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
 ATTCATGGCTGGAGGAGCTGTCACTCTCTCCGAGGATCTTACGGAGAGTGGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAA
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGAGGTTTCTTCTCTACAGCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC
 TGAGGCTGTATCCAGAGGGCCCAATATACCCACCTGCAGACCAGAGACCTACGAGGGGC
 TATGTCAGACCTGGGTTCACAGCCCACTCTCTACAGATCCCTAGCCTCTACTGTTCTCTAT
 GAGACCAATTCCAACGCCCTACCTGCTGCTCCAGCCATCCGGAAGGAGGTCTCCACCTGGA
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAATTAGAGAAC
 TTGCAGAACCATTGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG
 TACCGCATCAGCAAAAGTGCCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCTCAA
 CCACCGCATTTGCTGCCCTCACAGGCCTTGATGTCGCGCCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACATAATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC
 AGCCCCCTCTACAGAATGAAGTCAGGAACCCGAGTTGCAACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCCTGTGGTTAGGA
 ATGCAGCACTGTTTTGGTGGAAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCTGTCTCTGGTGGGAGATAAGTGGTGGCCAAACAGTGGATACATGAGTATGG
 ACAGGAATTCGCGAGACCCTGCAGCTCCAGCCCTGAAGACTGA**ACT**GTTGGCAGAGAGAAGC
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCACTTTGTCTGTGCCCTCGCAATCAGAGGC
 AAGGGAGAGGTTGTTACAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG
 AGTTCAGATACCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTTCGATCAGTGGGTC
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGCCTGACTCCCAACTTTAAGACTTTCTCCCACTGCCTTCTGCTGCAGCCCCAAG
 CAGGGAGTGTCCCCCTCCCAAGAAGCATATCCAGATGAGTGGTACATATATTAAGGATTTTT
 TTTAAGTTGAAAACACTTTCTTTCTTTTGTATGATGGTTTTTAAACAGTCATTAAAA
 ATGTTTATAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAAAGDTFSALTSVARALAPERRLGLLRRYLRGEEARL
 RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
 QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ
 VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
 LSREFLLYSPDNKRMAVNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS
 QPTLYQIPSLYCSYETNSNAYLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
 RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
 GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFIYANLSVPVVRNAALFWW
 NLHRSGEGSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSPED

Signal peptide:

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FIGURE 69

GAGATAGGGAGTCTGGGTTTAAGTTCCTGCTCCATCTCAGGAGCCCTGCTCCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
 ACGAGCGTGGCTGAGGGACCGAGCCGGAGAGCCCGGAGCCCCGTAACCCGCGCGGGGAG
 CGCCAGG**ATG**CCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
 TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGGCCCTGGTCTT
 GTCGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCTTGAAAGTGCCTTCC
 TGGCTCCAGCCATCATCCTCATCTCCTGGGCGTCTGTCATGTTTCATGGTCTCCTTCATTGGT
 GTGCTGGCGTCCCTCCGTGACAACTGTACCTTCTCCAAGCATTCATGTACATCCTTGGGAT
 CTGCTCATCATGGAGCTCATTTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
 ACTTCTTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAA
 AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
 GAGCAAGAATCAGTACCACGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA
 CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATATCGAC
 AAGGAGCGTTTCAGTGTGCAGGATGTCTACGTGCGGGGCTGCACCAACGCCGTGATCAT
 CTGGTTCATGGACAACATACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
 TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
 ATGCTGCTGTGTGTACCCAAAT**TAG**GGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCTGTGTGTAGTCCCACGGCCTCTGCCTC
 CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT
 GCCACCTGGGGCTGGGGAACAAGCCCTCCCTTCTCCAGGCCTGGGCTACAGGGGAGGGA
 GAGCCTGAGGCTCTGCTCAGGGCCATTTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA
 GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTTGGC
 CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGAGCCTA
 GTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC
 TAATCAAAGCTGGTATTTCCCGCATGTCTTATCTTGCCCTTCCCCAACCGATTGTGTTAA
 TCAACAATAAAAAATGTTTTGTTTTGTTTTTAAAAA

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863

><subunit 1 of 1, 294 aa, 1 stop

><MW: 33211, pI: 5.35, NX(S/T): 3

MPRGDSEQVRYCARFSYLWLKFSLIISTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AII LILLGVVMFMVSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPG PLACGVPTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAV IIFWMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDG LLGFGAKPSVEAAGTGCCLCYPN

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACCTTGCTGCCCTCTGA
 CACCTGGGAAGATGGCCGGCCCGTGGAACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACC
 TTGATCCAAGCCACCCTCAGTCCCCTGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAGA
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC
 GTCTTGAAGCACATCATCTGGCTGAAGGTCATCACAGTAACATCCTCCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACAGCCCCCTGGTCAAGACCATCGTGGAGTTCACATGACGACTGAGGCCCAAGCCACCATC
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
 ATCGAGGCTTCCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTT
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGTGACACCATT
 AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGAAAAGGTGACCAAGTGGTTCAATAAC
 TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA
 GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTCATGGTCCCTGTTGG
 ACTCTGTGCTTCTTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGTGGCCCACTGATCGTGTGGAAGTGTTCCTCCCA
 GTGAAGCCCTCCGCCCTTGTTCACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC
 ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCTATGGTG
 AAGGCCCTGGGATTCGAGGCAGCTGAGTCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
 AGCCTCCTTGTGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
 GGAAGGCTGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
 CAATAAACACTTGCTCTGTGAAAAA

FIGURE 72

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAM
REKPAGGIPVLGSLVNTVLKHIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRVLVSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYL
GAKLLDSQGKVTKWFNNSAASLTMPITLDNIPFSLIVSQDVKAAVAAVLSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGLIEASSEAQFYTKGDQLILNLNINISSDRIQLMNSGIGWGFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEESSLTKDALVLTASLWKPSSPVSQ

```

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATTGGTGGTGGCGCTG
 CTCATCGTTTGGCGACCTTCCCTCAGCCTCTGCCCAAAGAAAGAGGAGATGGTGTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTCCTCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTATCGTCATGTTCACTGCT
 CTCCAACATGCATAGACAGTGTGTGTTTGAAGCAAGCTGATGAAGAATCCAGATCCTGGC
 AAACCTCCTGGCGATACCTCAGTGCATTACCAACAGGATATTTTTGCCATGGTGGATTTTG
 ATGAAGGCTCTGATGATTTTTCAGATGCTAAACATGAATTAGCTCCAACCTTTCATCAACTTT
 CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC
 TGAGCAGATTGCCCGTGGATCGCCGACAGAAGTGTCAATATTAGAGTGATTAGACCCCC
 CAAATTATGCTGGTCCCTTATGTGGGATGCTTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTTGAAGAAGTAATATGGAATTTCTCTTAATAAACTGGATGGGCTTTTTCAGCTTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCACAGTTTGT
 GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGCCTTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG
 GACTTGTGTATTATTTCTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC
 CCATACAGCTTTCTGATGAGTTAAAAAGGTCAGAGATATATAGACACTGGAGTACTGGAA
 ATTTAAAAACGAAATCGTGTGTGTTTGAAGAAGAATGCAACTTGTATATTTTGTATTAC
 CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCCTGTCAAATCTGAGGTATTTGAAAATAAATTATCCCTCTTAACCTTCTCT
 CCCAGTGAACCTTATGGAACATTTAATTTAGTACAAATTAAGTATATTATAAAAAATGTAAAA
 CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAACACTACTTTAGTTAACTTGGTCACTGTAT
 TTTATATTGCCTTATCCAAAGATGGGGAAGTAAGTCCTGACCAGGTGTTCCACATATGCC
 TGTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT
 ACTTTACGCATCTTTCTTTTGTAGTAGAGAAATTATGTGTGTCATGTGGTCTTCTGAAAAATG
 GAACACCACTTCTCAGAGCACAGCTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT
 GCATATTTCTTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTTAACTACCTTGTATTTAGAAA
 GATTTAGATTCACTCCATCTCCTTAGTTTTCTTTAAGGTGACCCATCTGTGATAAAAAATA
 TAGCTTTAGTGCTAAAAATCAGTGTAACCTATACATGGCCATAAATGTTTCTACAAATTAGAGT
 TTGTCACTTATCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CAGGCGCAGTCACTTACGGCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTGAGGAGTTCGAGACCATCTGGCCAACATGGTGAACCCCGTCTCTACTAAAAATAT
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTTGAACCTCAGGAGATGGAGGTTTCACTGAGCCGAGATACGCCACTGCACCTCC
 AGCCTGCGAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLEWETNKRPVIRMNGDKFR
 RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
 SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
 AGPLMLGLLLVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
 PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLGMVLLCEATSDMDIGKRKIMCVAGIGLV
 VLFFSWMLSIFRSKYHGYPSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

FIGURE 76

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFDGRITFHPGSQVVKLPFFIN
MKTRGTSFLNAYTNSPICCPsRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVMVNLIRNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSFTHTSLYWLEKVS HDAIKIPKWSPLS
EMHPVDYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVII
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPL
PQNLSGSYLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAV

```

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATG
GCCTCTCTTGGCCTCCAACCTGTGGGCTACATCTTAGGCCTTCTGGGGCTTTTGGGCACACT
GGTTGCCATGCTGCTCCCCAGCTGGAACAAGTCTTATGTGGTGCCAGCATTGTGACAG
CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATACCCAG
TGTGACATCTATAGCACCTTCTGGGCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT
GGTGACATCCAGTGCAATCTCCTCCTGGCCTGCATTATCTCTGTGTGGGCATGAGATGCA
CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTT
ATCCTTGGAGGCCTCCTGGGATTCTTCTGTGGCTGGAATCTTCATGGGATCTACGGGA
CTTCTACTCACCCTGGTGCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTACTTGG
GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCTCTGCTTTTCTGCTCATCC
CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT
ATGTGTGAAAGAACAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
CACCCCGAGGGCCACAGGTGAGGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG
ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTCTGTTTTCTCACCTTGCTGCTC
CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCATTCCCTTAAGCCAGGACTCAGAGG
ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAACCCACTAATCACATCCCAGT
ACTGACCCTCTGTGATCAAAGACCTCTCTCTGGCTGAGGTTGGCTTGTAGCTCATTTGCTGG
GGATGGGAAGGAGAAGCAGCTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCCACCTTGTGTATGACTCCACAGTGTCC
AGACTAATTTGTGCTGAAGTGAATGAAATAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 78

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVG YILG LGLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFI PVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGIV
```

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

FMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC
 TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCCTGGCTCAG
 AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
 TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
 CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTTG
 TGAAGCTGAAGGTTCAGGGTGTGAATCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
 GAAAGCAGAAGACGTTTCCCTTGAGAAGACATAGAAAGAAAATCAACTTTCATAAGGCATC
 TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
 ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
 AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

1-10
 11-20
 21-30
 31-40
 41-50
 51-60
 61-70
 71-80
 81-90
 91-100
 101-110
 111-120
 121-130
 131-140
 141-150
 151-160
 161-170
 171-180
 181-190
 191-200

FIGURE 80

MVPRI FAPAYVSVCLLLCPREVIAPAGSEPWLCQPA PRCGDKIYNPLEQCCYND AIVSLSE
 TRQCGPPCTFWPCFELCCLDSFGLTND FVVKLVQGVNSQCHSSP ISSKCESRRRF

Signal peptide:

amino acids 1-25

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FIGURE 81

CTCCACTGCAACCAACCCAGAGCCATGGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
 TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
 GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT
 GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGAAACTGCACCTTCAGA
 GTCTGCTTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA
 CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTAATAATGGAACATCAGGGGAA
 CGATGACTCCTGGATTCTCCTTCCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
 TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACTCAACTGCCCACTTCATT
 CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG
 AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT
 GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCCTTACCCT
 TCTGTGAGATTTTCCATCATCTCAAGTTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
 TAAATTTATGTACTTTATAAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
 LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCD SARTSDDR LCRSVS

Signal peptide:

amino acids 1-24

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCGACGCGCTCACTCGCTCGCACTCAG
TCGCGGGAGGCTTCCCCGCGCCGGCCGCTCCCGCCCGCTCCCCGGCACCAGAAGTTCCCTCT
GCGCGTCCGACGGCGCA**CAT**GGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
TCCCTGCTCTTCGCTCTCTTCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTGCG
CACGCCGTATTCCCTGTATGTCTGTCCGAGGGGAGAACGTACCCCTCACCTGCAGGCTCT
TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCATCCGCAACCTCACGTTCCAGGACCTTCA
CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCCTGCTG
GATAGCGGCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACCTCGGAGCACAGGGT
CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGGTGT
ACCCATCCTCCTCCCAGGATAGTGAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
ATCGTAGGAATCCTCTGCCTCCCCCTCATCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
CTCCAACCGCGTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAAC
CCGGCTTTGAAGCCTCACACCTGCCAGGGGATACCGAGGCCAAAGTCAGGCACCCCTG
TCCTATGTGGCCAGCGGACGCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCACGAC
CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCTGTCCCTGACT
CTCCAAACTTTGAGGTCACT**TAG**CCCAGCTGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGCGCTCGGCCCTGGTTC
CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCAGCCCTCAACCCCTC
TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGTGCTGAG
ATTCTCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTCTGAGACATGAGCCTTGGGATGTGGCA
GCATCAGTGGGACAAGATGGACACTGGGGCACCTCCAGGCACCAGACACAGGGCACGGTG
GAGAGACTTCTCCCCGTGGCCGCCTTGGCTCCCCCGTTTGGCCAGGCTGCTCTTCTGTC
AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCGCTGCCCCACTGGCCATCGCC
ACCTTCCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
CTGGGGCTTCCATGCTGCATTCCAGTCCCCAGAGCTTGGTGGTCCGAAACGGGAAGTAC
ATATTGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
ATGTTTGCCCCACCACTGGAGATGGTGTCTGAGGAGGTGGGTGGGGCTTCTGGGAAGGTGA
GTGGAGAGGGGCACTGCCCCCGCCCTCCCCATCCCCTACTCCCACTGCTCAGCGCGGGCC
ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLFLFALFLAASLGPVAAAFKVATPYSLYVCPEGQNVTLTCRLLGVPDK
GHDVTFYKWTYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLSESAD
HHGNFSITMRNLTLGDSGLVCLVEIRHHHSEHRVHGAMELQVQTKGDAPSNCVVPSSSQ
DSENITAAALATGACIVGILCLPIILLYKQRQASNRRAQELVRMDNSIQIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSSEGRHLLSEPSTPLSPGPGDVFFPSLDVPDPSNFVEVI
```

amino acids 1-28

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
 TTCCCGCGGTTCTCTTTCCACCTTTCTCTTCTCCACCTTAGACCTCCCTTCTCGCCCTCC
 TTCTCTGCCACCGCTGCTTCTCGGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCTCCCCGA
 CTCGCTCCCGGACCAGCGGCTGACCCTGGGAAAGGATGGTTCCCGAGGTGAGGTCCTC
 TCCTCTTGTCTGGGACTCGCGCTGCTCTGGTTCCCTCTGGACTCCACGCTCGAGCCGCCC
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGCGCAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACTGCTCAGAGGGCGCCCATGTGAGT
 TGTTACCGCTCCACTGTCCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCC
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC
 CGCTGCCCAACCAAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
 AACCTGCCCCGAACCAAGGTGCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC
 CCCCCTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG
 GCAGCACAAGTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
 AAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCGTGCCTTCGGGCCCTTGCCCTG
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
 ACCCTTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCCAGAGGACAAA
 GCAGACCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGTCTCT
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGCTCGCTTGCCCTGGAACACGAGG
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCAC
 GAAGGTCACTGGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAAATAAAGAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

FIGURE 86

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGV RHPQDPCSSDAGRKRGP GTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGK TYSHGEVWHPAFRAFGFLPCILCTCEDGRQDCQ RVTCPT EYPCRHP EKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLP ERGTALPTARWPPRRSLERLPSDPG
AEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

[illegible]

amino acids 1-18

FIGURE 89

CAGGAGAGAAGGCACCGCCCCACCCCGCTCCAAAGCTAACCCCTCGGGCTTGAGGGGAAGA
 GGCTGACTGTACGTTCCCTTCTACTCTGGCACCAGCTCTCCAGGCTGCCATGGGGGCCAGCACC
 CCTCTCCTCATCTTGTTCCTTTTGTTCATGGTCGGGACCCCTCCAAGGACAGCAGCACCACCT
 TGTGGAGTACATGGAACGCCGACTAGCTGCTTTAGAGGAACGGCTGGCCAGTGGCAGGACC
 AGAGTAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAAGATGCTGCCACTGCTGGAG
 GTGGCAGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCGACACCATCTCCGGGAGAGTGGAA
 TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCAGCTCTGCCCTGTGTAGAGT
 TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAGGCAAGGGAAGAAGGAATGAGAAGTAC
 GATATGGTGACAGACTGTGGCTACACAATCTCTCAAGTGAGATCAATGAAGATTCTGAAGCG
 ATTTGGTGGCCAGCTGGTCTATGGACCAAGGATCCACTGGGGCAAAACAGAGAAGATCTACG
 TGTTAGATGGGACACAGAATGACACAGCCTTTGTCTTCCCAAGGCTGCGTGACTTCACCCCT
 GCCATGGCTGCCCGGAAAGCTTCCCGAGTCCGGGTGCCCTTCCCTGGGTAGGCACAGGGCA
 GCTGGTATATGGTGGCTTCTTTATTTTGTCTCGGAGGCCCTCTGGAAGACCTGGTGGAGGTG
 GTGAGATGGAGAACACTTTGCAGCTAATCAAATCCACCTGGCAAACCGAACAGTGGTGGAG
 AGCTCAGTATTTCCAGCAGAGGGGCTGATCCCCCCTACGGCTTGACAGCAGACACCTACAT
 CGACCTGGTAGCTGATGAGGAAGGTCTTTGGGCTGTCTATGCCACCCGGGAGGATGACAGGC
 ACTTGTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGGACACACCA
 TGTCCAGAGAGAATGCTGAGGCTGCCTTTGTTCATCTGTGGGACCCCTCTATGTCGTCTATAA
 CACCCGTCCTGCCAGTCGGGCGCCGATCCAGTGCTCCTTTGATGCCAGCGGCACCCGTAGCCC
 CTGAACGGGCAGCACTCCCTTATTTTCCCGCAGATATGGTGCCCATGCCAGCCTCCGCTAT
 AACCCCGGAGAACGCCAGCTCTATGCCTGGGATGATGGCTACCAGATTGTCTATAAGCTGGA
 GATGAGGAAGAAAGAGGAGGAGGTTTGAGGAGCTAGCCTTGTTTTTTGCATCTTCTCACTC
 CCATACATTTATATTATATCCCACTAAATTTCTTGTTCCTATTCTTCAAATGTGGGCCAG
 TTGTGGCTCAAATCCTCTATATTTTAGCCAATGGCAATCAAATCTTTCAGCTCCTTTGTT
 TCATACGGAACCTCCAGATCCTGAGTAATCCTTTTAGAGCCCCAAGAGTCAAAACCCCTCAATG
 TTCCTCCTGCTCTCCTGCCCATGTCAACAAATTTAGGCTAAGGATGCCCCAGACCCAGG
 GCTCTAACCTTGTATGCGGGCAGGCCCAGGGAGCAGGCAGAGTGTCTTCCCTCAGAGTG
 ACTTGGGAGGGAGAAAAAGGAGGAGACGTCCAGCTCTGTCTCTCTTCTCACTCCTCCCT
 TCAGTGTCTGAGGAACAGGACTTCTCCACATTGTTTTGTATTGCAACATTTTGCAATAAA
 AGGAAAAATCCACAAAAA
 AAAAAAAAAAAAAAAAAA

FIGURE 90

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLLIFLLSWGFLQQQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM
LPILLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVRFPPWVGTLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCIAKLDPQTLDEQ
QWDTPCPRENAEAAAFVICGTLVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV
```

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTCTCTCTAATCCAT
 CCGTCACCTCTCCTGTATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGAGGACGCAGCATTCTCCTGTTTCTGTCTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGCAGG
 ACAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCAGCTTTACTACAGAAGGCCA
 TCTGGGAGCTACAGGTGTCTAGCACTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTCTAGTCCTCGGGCTGGTTCCCCCGGGCCACAGCGAAGTG
 GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGTTACAGATAGGAGATACCTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCAATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGGAATAATCCAGGCGGAACCTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTGTAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGTGGACGGAGGACACAATAAAAGGTG
 GCGCGTGGGAGTGTCCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTCACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCTGCATGTCCGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTATAATGAGCAAAATGGAACCTCC
 ATAGTCATCTGCCAGTCAACCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
 AATCCAGAGACAAGCAACAGTGAGTCTCTCTCACAGGCAACCACGCCCTTCTCTCCAGGG
 GTGAAATG**TAGG**ATGAATCACATCCACATTCTTCTTTAGGGATATTAAGGCTCTCTCTCCA
 GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCTAGGTGCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATTTCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA
 AAAAAA

FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFCFLSPKTNAEAMEVRFFRGQFSS
 VVHLYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYYQK
 AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFRPTAKWKGPQGDLSTDSRTNRDMH
 GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTTFEPISWHLATKVLGILCCGLF
 FGIVGLKIFFSKFQWKIQAELDWRKKGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT
 HRKAPQEVPHSEKRFTRKSVVASQSFQAGKHYWEVDGGHNRWRVGVCRDDVDRRKEYVTLS
 PDHGYWVLRNLNGEHLTYFLNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQS LIYTLTC
 RFEGLLRPYIEYPSYNEQNGTFIVICPVTQSESEKASWQRASAI PETSNSSESSQATTPFLP
 RGEN

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGC GCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTTCGGATTGCA
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGAGCCGAGCGCGC
CATGAGGAGCCTGCCAGCCTGGCGGCCCTCGCCCTGTGTGCTGGCGCCGCCGCCGCCGCCG
 CCGTGCCTCAGCCGCTCGGCGGGGAATGTCACCGGTGGCGGCGGGGCCGCGGGGCGAGGTG
 GACCGCTCGCCGGGCCCCGGGTTCGGGGGCGAGCCGACCCCTTCCTTAGGGCGACGGC
 TCCCAGGGCCAGGCCCGGAGGACCGGGCCCCCGCGGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCAGTCCCGGAGACCACCCCTCTTTGGCGACTGCTGGACCCTCTTCC
 ACCACCTTTAGGCGCCGCTCGGCCCTCGCCGACACCCCTCCGGCGCGGAACGCACCTTC
 GACCACCTCTCAGGCGCCGACGACACCCGCGCCGACACCCCTTCGACGACCACTGGCCCGG
 CGCCGACACCCCTGTAGCGACACCGTACCGCGGCCACGACTCCCGGACCCCGACCCCG
 GATCTCCCAGCAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCCCTC
 TTCGCTCTCTCAGAGTATGTATGTAACCTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACC
 TGCAAAGAGGGCTTTACCTAAATTACACTTCTGGGCTCTGTACGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAACTGAAGTTTATT
 TTATTTTAGCAAGGGAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
 GAGGATGAGGTCATAGATTTACAAAATATTTTATATACTTTTATCTCTACTTTTATATGT
 TATATTTAATGTCAAGATTTAAACATCTAATTTACTGATTTAGTCTCTCAAAGCAGTAG
 AGTCGCCAATTTTCTCTGGGATAATTTCTGTAATTTTCATGGGAAAAAATTAITGAAGAAT
 AAATCTGCTTTCTGGAAGGGCTTTGAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT
 ATGTTTATTAATATACCATTTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTCTCTCTA
 ATCAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCTAATTTA
 TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTATACAGTACATTTTGGAGCCAAAAG
 TAGATTAAGCAGGAATATCTTTAAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGG
 ATAATGACTGTTTATCTAAGCATTTGCCCTGTACTGCAGTGAAGTAATTTATCTTTGACCT
 TATGTGAGGCACTTGGCTTTTGTGGACCCCAAGTCAAAAACCTGAAGACAGATATTAAT
 AATGAAAAAATAATGACAGGTTATATACTAGTGAACCTGGGTATACCCCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCCCTGGGCAAGTAATTTCCCTTCACTGAGCTTGTCTCTCTCAAG
 GTTGTGTGAAGATTAATGAGTGTATATATAAAATGCCTAGCACATGTCACTCAATAAA
 TTCTGTTTGTTTTAATTTCAAAGGAATATTATGGACTGAATGAGAGAACATGTTTAAAGA
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTATACTTTAGCACTAAATATTTTAAATGCTTTA
 TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCACCCCTGTAATCCTAGCACTTTGGGAGGCCAAGCGGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACCCCGCTCTACTAAA
 AATACAAACAAATAGCTGGGCGTGGTGGCACACACCTGTAGTCCGACTACTCGGAGGCT
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAAGTGAAGTGAAGTGAAG
 GCACTCCAGCCTGTGTAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 94

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSPLGGLALLCCAAAAAASASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPWLWATAGPSSTTFQAPLGPSP TTPPAERTS
TTSQAPTRPAPTTLSTTTGFPATTPVATTVPAPTTPTPTDLPSSSNSSVLPTPPATEAPS
SPPPEYVCNCSSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLN YTSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCAGGCCGTGTGGTTGGGAAGACTGGACCTTGAGCAGCTTCTTGGG
CCCTTGGTACGTGCTTGCAGTGGCCTCCCGGGAAAAGGCGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGACCTCACTCCAGAAAAACACCTGCGGACGCTGTCTCTC
AGCACGGGCTGGGAGGCTGTGACCAGAGTGTATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAGTGGAGCAGGAGC
CTGGGCTTCTGTGTCAGTTAGCAGGCCAGCTGCAGAAAGACCTCACTGTGCTCACAAGAT
CCTTCTGTGAGTGCTGCGTCCCACTAGGGGATGGCGGCCACAGGGTCCGTGTGACCTCGGCCA
GTGTCACCCACCTCGCTCAGCGGCTCCGGGGGCCAGCACACAGCTCAGAATAAAGCGATTTC
CACAGCA

FIGURE 96

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
 LTPENNLRTLSSQHGLGGCDQSVMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL
 EFGDEFFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

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100

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGAC**ATG**CTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGACAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
 GGCTGGATTTACCCTGGCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGA
 CCAGGATGCTCCAGTGCCACAAACAACCCAGCTCGGGCAGTGTTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCTTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGAGATACTTCTTTCTGATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATACCCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
 GCACCTGGAGTCCGGCTGCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
 GGGACACCCCTATGATCTCTCGGATAGGGACCTCCGCTGTCCCCCTGGACCCCTCCACCAC
 CCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC
 CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCCTGACCTGTGCCCC
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
 ATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTGGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCTGTCTTCTGCGTCATCTTCTGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTCAGCCT
 CTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCAGCT
 TCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCAGTACTCGGAGATCAAGATCC
 ACAGAT**CGA**GAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCCTCAGGCAAGGGA
 GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTTATTTTTAACTAAAGACAGACAAATTCCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF
 REGANTDQDAPVATNNPARAVWEETRDRLFLLGDPHTKNTLSIRDARRSDAGRYFFRMEKG
 SIKWNYKHHRLSVNVTALTHRPNILIPGTLES GCPQNLTCVFPWACEQGTPPMISWIGTSVS
 PLDPSTTRSSVLTLPQPQDHGTS LTCQVTFPGASVTTNKTVHLNVSYPPQNLTMTVFQGDG
 TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
 HLRDAAEFTCRAQNPLGSQQVYLVNLSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
 CRKKSARPAAGVGDTGIEDANAVRG SASQGPLTEFWAEDSPPDQPPASARSSVGE GELQYA
 SL SFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTCTCTG
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCTTCACCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTCCGGAGGACAGGAGGCCAGGA
AGGTGTCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTCACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGAGGCCCTGGAAGAAATTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTCAGCCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTTAGG
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT
TTTCCCCCAA

FIGURE 100

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTFLGVTGLGLAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSFVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

```

Important features:**Signal peptide:**

amino acids 1-17

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
 TCCTGCTTGTCTTGGCAACAGGGCTTGAGGGGAGAGACCAGGATCATCAAGGGGTTTCGAG
 TGCAAGCCTCACTCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG
 GCGGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
 TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTTCCCCACCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
 CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
 AGCCCCCAGTTACGCCTGCCTCACACCTTGCATGCGCCAACATCACCATCATTGAGCACCA
 GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
 AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTT
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
 GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA
 CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTGTTGGTTCCTGTTCACTCTGTTAAT
 AAGAAACCCTAAGCCAAGACCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
 CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCGCTT
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTTCTCTGTTGTATCCCCAGCCCCA
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTGCTAAATGAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRIYIVHLGQHNLLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIEHQKCENAYPGNITDTM
VCASVQEGGKDSQGDSCGGPLVCNQLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

```

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTCTCTGCTGGAGCCG**ATG**CCAAAAACCATGCATTTCTTATTACAGATTCATTGTTT
 TCTTTTATCTGTGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA
 GTGAAAAATAGAAGTTTTGCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT
 ACTAAATGCCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTTCTACTGCAGCCGGA
 CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA
 GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
 TGCATACGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG
 AGATTGAACTTTATGCTGTGACCAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
 ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
 AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTTAAGA
 AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT
 GAACTA**TAG**CATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
 AAACAAAGTCACTTTCTCCAAGTTGTATTTGCTATTTTCCCCATGAGAAGATATTTTGA
 TCTCCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTGCAAACTTAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEIDIFKKNHDHGDGFISPKYENVYQHDEL

```

Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCCTGCTTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAAACAAAACCTTCCTGTGCTAAGTGCCCCCAAATGCTTCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAAACATTACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTGAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAAGTCAAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACCTCCAGCATGGATGACAGAGCAAGACTCCGTCCTAAAAAGAAAAGA
TAGTTTCTTGTTTCATTTGCGGACTGCCCTCTCAGTGTTTCTGGGATCCCCTCCCAATAA
AGTACTTATATTCTC

FIGURE 106

MQGPLLLPGLCFLLSLFGAVTQKTKTSCAKCPNASCVNNTHTCTCNHGYTSGSGQKLFTFPL
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FIGURE 107

CAAGCAGGTCATCCCCTTGTTGACCTTCAAAGAGAAGCAGAGAGGGGCAGAGGTGGGGGGGCAC
 AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGG**
 GGCTCAGCATCTTTTTGCTCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
 CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA
 GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
 CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA
 CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC
 CCTGCCCTGCCAATGACTGTGCAACCGCTGGCACCAGGTGCCACGTCTCAGGCTGGGGC
 ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTGTATCCCAGGAGAATCACGAGCAACATGGTGTGTGCGAG
 GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
 GTCCTTCAAGGTCTGGTGTCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC**TGAC**
 CTGTTTCTCCACCTCCACCCCAACCCCTTAACCTGGGTACCCCTCTGGCCCTCAGAGCACC
 AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTGGCCTGGGAACCTCTTGGAACCTT
 TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSSV
 QFLPLPNDCATAGTECHVSGWGITNHPNPFDDLQCLNLSIVSHATCHGVYPGRITSNMVC
 AGGVPGQDACQGDSSGGPLVCGGVLQGLVSWGSGVPCGQDGIPGVYTYICKYVDWIRMIMRNN

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FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATGT**CGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGGAAGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC
 GAGATCAACCGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCAGAAAA
 GCTCAGACCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
 TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTACACTATATCCTACCGAGACTTTGTGAA
 CATGATGCTGGGGAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**
 GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTGTTGTTT
 TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGGGGAATCC
 TGAGCCTTGGGTCCCCCTCCTCTCTTCTTCCCTCCTTCCCGCTCCCTGTGCAGAAGGGCTG
 ATATCAAACCAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCT
 CTCATTGGAGGAACAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGAGTAGGGACAAGG
 CTGCAGGGCTCTTTCGGGTTTCTTGACAGTGCCATGGTCCAGTGCTCTGGTGTCAACC
 AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCACACCTCTTCT
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
 TACCAGAAGGAACCTCCAGTCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGACGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG
 GGGTTTGGGGGGAAGGTGAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
 CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGTTGCTTGCTGTGACCCCAATCTGCTTGAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
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FIGURE 111A

CGCGCTCCCCGCGCGCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA
GGAGCGGGGCCCTGCAACACATGCCCCCGGGTGGGCAGGGGTGCGCGCCCGCGTGCAGCGCC
CGCTTGGCGCTGGCCTTGGCGCTGGCAGCGTCTTGAAGTGGGCTTCCAGCCCTGCGCTGCC
CACCAAGTGTACCTGTCTCCGTGCCAGCGTGGACTGCCACGGGCTGGGCTCCGCGCGGTTC
CTCGGGGATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAAGGATC
ACCAAGATTGGAATTTCCGTGGGCTCAAGAACCCTCCGAGTCTTGCACTTGGGAAGACAACAGGT
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCTGAACA
AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA
GATTTGAGTGAACACAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCGATGT
GAAGAACCCTGCAACTGGACAACAACCATCATCAGTGCATTGAAGATGGAGCCTTCCGAGCGC
TGC GCGATTGGAGATCCTTACCTCAACAACAACAACATCAGTCGCATCCTGGTCACCAGC
TTCACCCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACTCTACTGCGACTG
CCACTGCGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTTACACTCT
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCGAGAAGAAGGAGTACGTG
TGCCAGCCCCCACTCGGAGCCCCCATCCTGCAATGCCAACTCCATCTCTGCGCCTTTCGCC
CTGCACTGTGACGCAATAACATCTGGACTGTGAGGAAAGGGCTTGATGGAGATTCTTGCCA
ACTTTCGGGAGGGCATCGTTCGAAATACGCTTAGAACAGAACTCCATCAAAGGCATCCCTGCA
GGAGCCTTCAACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCCGA
TATTGCTCCAGATGCTTCCAGGCGCTGAAATCACTACATCGCTGCTTATGGGAACA
AGATCACCGAGATTGCCAAGGGGACTGTTGATGGGCTGGGTGCTCCCTACAGCTGCTCCTCCTC
AATGCCAACAGATCAACTGCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTTCGCCCTCTGTCAGT
CCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCGCCGCTGCAGCAGCCCGCGCGC
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
ATTACCGCAGCAGGTTTTCAGCAGCGAGTGTCTCATGGACCTCGTGTGCCCGAGAAAGTGTGCG
TGTGAGGGCAGCATTTGTGGACTGCTCCAACCAAGAAGCTGGTCCGCATCCCAAGCCACTCCC
TGAATATGTACCCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
TCTTCAAGAAGTTGCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCGAGGAGCTGATGCTGACAGGGAACCACT
GGAGACCGTGCAGGGGCGCTGTTCCGTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA
GTAACCTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCGCTGAGACTGCTG
TCCCTCTATGACAAATCCGATCACCACCATCACCCTTGGGGCTTACCACGCTTGTCTCCCT
GTCCACCTATAAACCCTCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
AGTGGTTGAGGAAGAGCGGATCGTCACTGAGGAAACCTTAGTGCCAGAGCCACTTTTCTCTC
AAGGAGATTCCATCCAGGATGTGGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAG
TAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGGAT
CGAGCAACAAGGGGCTCAGCGGCCCTCCCGAGGGCATGCCAAGGATGTGACCGAGCTGTAC
CTGGAAGGAAACCACTTAACAGCCGTGCCAGAGAGCTGTCCGCGCTCCGACACCTTGACGCT
TATTGACCTGAGCACAACACCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCGTCCACGCCTTCAAC
GGGCTGCGGTCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTCTCTGAAGG
CTCTTCAACGACCTCACATCTCTTCCCATCTGGCGCTGGGAACCAACCCACTCACTGTG
ACTGCACTCTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC
CGCTGCAGTAGCCCTGAGCCATGGCTGACAGGCTCCTGCTCACCAACCAACCCACCGCTT
CAAGTGCAAAGGGCCAGTGACATCAACATTTGGCCAAATGCAATGCTGCTCTCCAGCC
CGTCAAGAAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCTGCCCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCCATCAACACCTGCATCCAGAACCCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTTCAGTGTCTCTGCCCTC
 TGGGCTTTGAGGGGACGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
 AACATGCCACCTGCGTGGACGGGATCAACAACACGTGTGTATCTGTCCGCTAACTACAC
 AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTACGATG
 AGGCCAAGTGTCATCCCCCTGGACAAAGGATTTCAGCTGCGAGTGTGTCCCTGGCTACACGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCACAAGTGCCGCCACGGGGCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCCTTCTGTG
 AACACCCCCACCCATGGTCCTACTGCGAGCCAGCCCATGCGACCACTACGAGTGCCAGAAC
 GGGGCCCAGTGTCATCGTGGTGACGAGGAGCCCACTGCCGTGCCACCAAGGCTTCGCCGG
 CCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAGACTCCTACGTGGAACCTGG
 CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC
 GGCATCCTTCTCTACAAAGGAGACAATGACCCCTTGGCACTGGAGCTGTACCAGGGCCACGT
 GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCACAGTGTACAGTGTGGAGACAGTGA
 ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCCTGAACCTAGTAGTG
 GACAAAGGAACCTCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCTCTCCGCTTGCGCCAGGGCACGG
 ACCGGCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAC
 GACTTCAAGGCCCTCCACCAACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCTGCACCGT
 GTGCAAGCACGGCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG
 GCTGGACCGGCCCCACTCTGCGACCAAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC
 CATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG
 GGACTTGTGTGACAACAAGATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTACCATG
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC
 GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCTGGGGGCT
 GTGGGCCCCAGTGCTGCCAGCCCCACCGCAGCAAGCGCGGAAATACGCTCTTCCAGTGCAAG
 GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC
CTAAGCCCCCTGCCCGCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
 ATGTGGGACCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA
 AGAGAATATTAAGTATATTGTAAATAAACAAAAAATAGAACTTAAAAAAAAAAAAAAAAA
 AAAAA

FIGURE 112

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLRNNITRITKMDFAGLKNLRVLHLEDNQSVIERGAFQDLKQLERLRLNKNKLQVL
 PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRI LVSFNHMPKIRTLRLHSNHLCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFQYKKLKRIDISKNI SDIADAFQGLKSLTSLVLVGNKITEIAK
 GLFDGLVSLQLLLL NANKINCLRVNTFQDLQNLNLLSLYDNKLQTI SKGLFAPLQSIQTLHL
 AQNPFCVDCCHLKWLDADYLDNPIETSGARCSSPRRLANKRISQIKSKKFKRCSGSEDYRSRFS
 SECFMDLVCEPKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRRLNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
 SNDTFAGLSSVRLLSLYDNRIITITPGAFTTLVSLSTINLLSNPFCNCHLAWLGKWLKRKR
 IVSGNPRCQKPFLLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGLR
 ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLIL
 SYNRLRCIPVHAFNGRLSLRVLTLHGNDISSVPEGSFNDLTLSHLALGTNPLHCDCSLRWL
 SEWVKAGYKEPGIARCSSEPEMADRLLLTTPTHRFPQCKGPDVINIVAKNACLSSPCKNNGT
 CTQDPVELYRCACPYSYKGDCTVPINTCIQNPCQHGGTCHLSDSHKGDFSCSCPLGFEGQR
 CEINPDCCEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVPELNLQHEAKCIPL
 DKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDITINGYTCTCPQGFSGPFCEHPPPMV
 LLQTSPCDQYECQNAQCIVVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS
 VELVLTNLQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIEHVRINNELQDFKALPPQSLGVS PGCKSCTVCKHGLCRSVEKDSVVECEPRGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKNDSANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVI RQKGYASCATASKVPIMECRGGCGPQQCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTCCTTCGCA
 GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
 CCGGCAGGCTTTGAGG**ATGA**AGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG
 GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG
 GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA
 CAACACCACAGCCCCGACGGTCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
 ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGC
 TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATGTTTAAAGA
 GACACAAGGAATGAACATATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
 AGTGGAaaaaaaggctgtgaggtttcc**TAA**ACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC
 GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCTTTCTCCCAATA
 TTCCTTCTCAAACCTGGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAAATAAATATTTCCAT
 TTAAATGTC

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 100
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 70
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 40
 30
 20
 10
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Signal peptide:
amino acids 1-19

[illegible]

FIGURE 115

CAGGCCATTGTCATCCCACTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCATTAAAACTTGTACATGGCTCCC
 CATTGGTTTTTGGAGAAAAGTTCAAGCTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACCTCCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTACAGCTGCTGTTTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCTGATGTCCCTATCCATCTCTAAATGTCACCAG
 CTTTGACTCAGTTGTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCTGTC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC
 CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCCAAGTCATTGCTGTTAATTCGGGTGGACCTTGGAGT
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACTTCTCAGAAGCA
 ATAGAAAAGTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTTCCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGAT**TAA**TCAGATTGTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC
 CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAA
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACCTCCCTGTCCACTTTTCAGAAA
 AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTTCAGCAGAGTATTTAATTATATTTTCTCGGGATTATTGCTCTCTGTCTA
 TAAATTTGAATGATCTGTGCCTTAATTGGTTTTCATAGTTAAGTGTGTATCATTATCAA
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTCCCAGATTCAAT
 CCACCGAAGTGTTCACTGTCATCTGTTAGGGAATTTTTGTTTGTCTGTCTTTGCCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTTTTAAGATAAATTTGTATTTTGCACACTGAGATATAA
 TAAAAGGTGTTTATCATAAAAA

FIGURE 116

MPLLKL VHGSPLVFGEKFKLFTLV SACIPV FRLARRRKILFYCHFPDLLLT KRDSFLKRLY
 RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
 DLVPGKGGKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
 HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
 IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
 TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCA**ATG**TTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCAGAC
 AAGCTGCAGGAATCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT
 CTCCTTCTGGTTTGGCAGGCGCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCCTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAATGGTGT
 GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTG
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAGGCTTTCTAGATGGGTCAC
 TTGATAAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAGAACGAAAGGAAGGAACCTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCCGTGTTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAAACTGTTGCAACTGCCA
 AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATATTATT
 CCTAGAGAGACCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAACCTTTTCCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA
 AACAAAGTATGAAGTGGTAACATCATCAAGGGAAGAAGCTTGGATCAGTGTCTCAAAGAGAT
 AT**TAAA**ATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAAA
 AAATCTATGTTGAATCCTTTTATAAACCAGTATCACTTTGTAATATAAACACCTATTTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
 ERYGPVVSFWFGRRLVVSIGTVDVLLKQHINPNKTSDPFETMLKSLLRYQSGGGSVSENHMRK
 KLYENGVTDSLKSNFALLKLSEELLDKWLSPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
 DDQEVIRFQKNHGTVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
 QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLTSEEVQKKLYEEINQVF
 GNGPVTPEKIEQLRYCQHVLCE TVRTAKLTPVSAQLQDIEGKIDRFIIPRET LVLYALGVVL
 QDPNTWPSPHKFDPDRFDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS
 VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTTGTGCGCTTGC GGGGAGACTTCAGGAGTCGCTGTCTCTGAACTCCAGCCTCAGA
 GACCGCCGCCCTTGTCCCCGAGGGCCATGGCCCGGTCTCAGGGCTTGTGCCCTCTCGCTTC
 CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT
 ACAGGCCTGCCTGCCTCTCACGTTCACCCCGAGGAGTATGACAAGCAGGACATTAGCTGG
 TGGCCGCGCTCTCTGTACCCTGGGCCTCTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
 GTCTCCATGTTCAACAGCACCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
 GGCCCTGTCTTCTTCATATTCGAGCGTTGGGAGTGCCTACGTATTGGTACATTTTGTCT
 TCTGCAGTGCCTTCCAGCTGTCACTGAAATGGCTTTATTCTCACCGCTCTTTGGGCTGAAA
 AAGAAACCCCTTCTTGATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
 CCGCTTCGTATTCTTGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC
 TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
 GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA
 ATTA

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

FIGURE 121

TCCCGGACCTGCCGCCCTGCCACT**TATG**TCCC GCGCTCTATGCTGCTTGCCTGGGCTCTCC
 CCAGCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
 GTGCCCCGGAACGAGTGGAAAGGCCCTGGCATCAGAGTGC GCCCAGCACCTGAGCCTGCCCTT
 ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGTGC AACACCCCGCCTCGTGCCAGC
 AGCAGGCCCCGGAATGTGCAGCACTACCACATGAAGCACTGGGCTGGTGCACGTGGGCTAC
 AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGA ACTTCACGGGTGC
 CCACTCAGGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
 ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT
 CAGGGAGCCCTGAGGTCCA ACTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
 TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TG**AGGCC
 CTGCTGATCCGCACCCCATTCCTCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA
 ATAAAGATGTAGCTC

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FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
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FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT
 GACTCGCTGCTGCTTCGTGTTCTCGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCTCTCCCGCTCAGAGGACCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
 CGGGTGCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCATGGCCAATTCCACTCT
 CCTAGGGTGTGTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCCGCGGACCTC
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGTGTCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACTACCATAGTGATACCCCTACTACCCATC
 TGGG**TGA**CCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTTGGGCCTCAGGCAGGGAGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG
 CTGGTCCC**AAC**CTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCTTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCTTAGGAGCCAGTCAGCAGGGTGGGTGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCC
 ACAGCCCATCCGCGTGTGTGTGTCCCTCTCCACCCCAACCCCTGTGTGGCTCCTCTGGGAG
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGTGGGGCGGGCCGGGCCGAGA
 GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGTGGGGGAGGGGAGGGAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGAGACAGGAAATAAAGCTT
 GCCCCGGGGCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVCPTYNYHSDTPY
YPSG
```

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAAGAGTGGGTGCAGGGGCCCA
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
 TGGTGGAAGTGTGCGCGCCGCCGCGCTCGTCTCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCGAGCACCGGGATCCCGGGTAGGAGCGACGCGGGCGAGCACACGCGCCAGCC
 GGCTCGGGTGCCACACAGGCTCACCATGGGCTCCGGGCGCGGGCGCTGTCCGCGGTGCCG
 GCCGTGCTGCTGGTCCTCACGCTGCCGGGGCTGCCGTCTGGGACAGAACGACACGGAGCC
 CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGCGACTCGAACCCGGCCACGGACTCCAAGG
 GCTCCTCTTCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTGCGCTTCTCG
 GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
 CGATCAGATCCTGGTGAATGTGGGTAATTTTTTCACATTGGAGTCTGTCTTTGTAGCACCAA
 GAAAAGGAATTTACAGTTTCAGTTTTCACGTGATTAAAGTCTACCAAGCCAAACTATCCAG
 GTTAACTTGATGTTAAATGAAAACCAAGTAAATATCTGCCTTTCGGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATCCACGTTTTCTGGCTTCTGGTG
 TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCAATTTCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTGTTTAGTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACCTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
 TGTTAATATATTGATTATATTTGTTTTATTCTTTTGAATTAGTTTGTTGGTTCTTGTA
 AAACTTGGAATTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAAAAAGGTAATGAA
 TGGCTTGCCACAAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAA
 GAATGCTTCATAGTTGTATTTTAAATGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
 TTCTAAGAAGAAGATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCTCCGAGGGAATCTTATACTTTATTGC
 TCAACTTTAATTAAAATGATTGATAATAACCACTTTATTA AAAACCTAAGGTTTTTTTTTT
 TCCGTAGACATGACCACTTTATTAACCTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
 TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA
 TATATTTATCTGTTTAGCTAATATTA AATTCAAATATCCCATATCTAAATTTAGTGAATAT
 CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAAA

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FIGURE 127

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTCGTCCTTGTTGGTTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCTTTATTCAGCTTTCATGAC
GCTGGTCATTATCTTGCTGCAATGATTCTGGGGCATTGTATTTTTTGTGAGTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTTATAATCCTGGTGTCTATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTTTTACAACCGCGCTCCAGAT**TAA**CCCTCAGGGAACAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 128

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFTAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGPGTVGIHGDSFPQFFLYSAFMTLVIIILHVFVGIVFFDGCCKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKN
FLLYNQRSR
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACACGACCGCCGCCACCAACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTGCTGCTGGGCTTGCCCTTCT
 TGGTGCTCTTGGTGGCTCGGTGAGAGCCATCTGGGGGTTTGGGGCCCAAGAACGCTCTCGCAAGAAACGCGCG
 AGTTTGAAGCGACCTACGCTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATCTGTGACCC
 GCAACAGGACAGAGGGCGTGCCTGTGTCTGTAACGCTCCTGAACAGCAGAGGGGGCGCGTGTCTGTTTGTGG
 TCGCCAGAAAGAGGCTGTGGTGTCTTCCAGGTGCCCTAATCTCGAGGGATGTTTTCAGCGCAAGTACCTCT
 ACCAAAAAGTGGAAACGAACCTGTGTGAGCCCCCACCAGAATGAGTCGGAGATTGAGTCTTCTACGTGGATG
 TGTCCACCTGTACCAAGTCAACACACATACCAAGCTCCGGGTGAGCCGATGGACGATTTTGTGCTCAGGACTG
 GGGAGCAGTTCAGCTTCAATACCAAGCAGCAGCAGCCCCAGTACTTCAAGTATGAGTTCCTGAAGGCGTGACCT
 CGTAATTTGTCAAGGTGACTCCACCAAGGCCCTTCCCTGCTCAGTCTATCCATCCAGTGTGCTGTGTCTCTG
 TCTATGACCTGGACACAACTGAGCCTTTCATCGGCATGTACCAAGACGATGACCAAGAAGGCGGCCATCACCCTGAC
 AGCGCAAGACTTCCCCAGCAACAGCTTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGGCT
 CCGTGCCCTTTCACCCCTTCGCAGAAAGTGAACCGGTCGATCAAGGGCACCGCCAGAAACCCCTGTCTGCTGTGG
 TGTCTCAAGCAGTCAAGCTGAGGCATACGTCAGTGGGATGCTCTTTGCTGGGTATATTTCTCTCCTTTTACCC
 CTGTGACCGTCTCTGGCTGCTGGGAGAACTGGAGGCAGAGAAGAAGACCTGCTGTGGGCATTGACCGAG
 CCGCCCAAGAACGGTCAACCTCGAGTCTGGCTGATTCTTTCTGGCAGTTCCTTTATGAGGTTTACAAT
 ATGGCTCCTTTGAGAATTTTCTGGATCTACCGATGGTCTGGTGAACAGCGCTGGACCTGGGACCTCTCTTACG
 GTTACCAAGGGCGCTCTTGAAGCTTAGGTAAGTCTGGGCGCCGAGTGCATGAGCTCTGTGAGGAGGATG
 ACTACAGACATTTGGCCGACATCGATTCCGACAAGAAATGTATTCGCAACCAAGCAATACCTCTATGTGSGCTGACC
 TGGCAGGGAAGGACAGCGCTGTTCTGGGAAAAAGTACCGATCTACTTCTGGAACAGTTCGCCACCTTGTGCTGT
 TCTATGCCCTTCTGTGGTGAAGCTGGTGATCACTACCAAGCGGTGGTGAATGTACAGAGGATGACGACATCT
 GCTACTACAACCTTCTCTGCCGCCACCACTGGGCAATCTCAGCGCCTTCAACCAACCTCTCAGCAACCTGGGGT
 ACATCTCTCTGGGGCTGTTTTCCTGCTCATCATCTGCAACGGGAGATCAACCAACCGCGGCTGCTGCGCA
 ATGACCTCTGTGCGCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTAGCGCATGGGCAAGCCCTGATGA
 TGGAGGGCTGCTCACTTCTGCTATCATGTGCGCCCAACTATACCAATTCAGTTTGAACACATCGTTCATGT
 ACATGATCGCGGACTGCTGATGCTGAAGCTCTACCAAGCGGCAACCCGAGCATCAACGCCACGGCTACAGTG
 CCTACGCTGCTGCCATTGTATCTTCTCTGTGTGGGCGTGGTCTTTGGCAAGGGAACACGGCGTCTT
 GGATCGTCTTCTCATCATTTACATCATCGCCACCCCTGCTCCTCAGCAGCGAGCTCTATTACATGGGCGGTGGA
 AACTGGAATCGGGGATCTCCGCGGCATCTCCACGTGCTCTACACAGACTGCATCCGGGATGCGAGCGGGCCG
 TCTACGTGGACCGGATGGTGTGCTGGTGTGATGGGCAACGTCATCAACTGGTGTGCTGGCTGCTATGGGCTTATCA
 TGCGCCCAATGATTTCGCTTCTACTTTGTCGCAATTGGCATCTGCAACCTGCTCCTTTATTCGCTTCTTACA
 TCTATCATGAAGCTCCGGATGGGGAGAGGATCAAGCTCATCCCTGCTCTGCACTCGTTTGACCTCCGTGTGCT
 GGGGCTTCGCGCTCTTCTTCTTCTCCAGGACTCAGCACTGGCAGAAACCCCTGCAGAGTCGAGGGAGCACA
 ACCGGGACTGCATCTCTCTCACTTCTTTGACGACACGACATCTGGCACTTCTCTCTCCATCGCCATGTTCG
 GGTCTTCTCTGGTGTGTGACACTGGATGACGACCTGGATCTGTGCAAGCGGACAAGATCTATGCTTCTTAGC
 AGGAGCTGGGCCCTTCTGCTTCACTCAAGGGGCCCTGAGCTCCTTTGTGTATAGACCGGCTCACTGTGTGCTGT
 GTGGGGATGAGTCCAGCACCCTGCCACGACTGGATGGCAGCAGGACAGCAGCTGTAGCTTAGGCTTGGGCT
 GGGACAGCCATGGGTGTCGATGGAACCTTGACGCTGCCCTCTGCCAGGAGCAGGCGCTGCTCCCTGGAACCCCC
 AGATGTTGGCCAAATGCTGCTTTCTTCTCAGTGTGGGGCTTCCATGGGCGCTGCTCCTTTGCTCTCCATT
 TGCTTTCTCAAGAGGAAGGATGAAGGGACACCTCCCAATTTCATGCTTGCATTTTGGCCGCTCTCTCTCCCC
 ACATGCCCCAGCTGGGACCTGGAAGGCTCTTTTCTTCCCACTACTCCCATCCAGGGCTAGTCTGGGGCTGGA
 ATCTCTGTCTGTATCAGGGCCCCAGTCTCTTTGGGCTGTCCCTGGCTGCCATCTGCTGCTTCCAGTCTGAGG
 AGGATGGATGGGGGATGAGATTTTGGGGGTGGCCAGCTGTGGCAGCTTTTGTGCTAAGGCTGCAAGGG
 CCTGGGGCATGCGATTTCTTCTTCTGACCTGTGCTCAGGGCTGGCTTTTGAACAATGCGCTGACGCCAAT
 TGAGAAGCGCTCTGATGACAGAGGCTGAATTCAGAGGTCACCTTCTATCCATCAGCTCCAGCACTGATGCC
 AGCACAGGACTGGAAGGAGAGCGCTCAACCCCTTCCCTTCTTCCAGGCGCTTAGTCTTCCCAACCC
 AGCTGTGGGCTTGCATGCCATTGACATCTGACATCTCCAGGCAAGAGGATGATACAGATGTCAG
 CCGCTTCTGCTCCACAGCTGTGGGACCCAGTGCCTTACCTTGAAGAGGGCTCAGGAAGGATGTGCTGTTT
 CCCTCTAGCTGCCAGTCTGCTAGCTCCTCTAGAGCCAGGCTGGCTTCTAAGTTTCCGTCAGCTTCCAGGA
 AGTTCTGTGTAGTCATGSCACACATACCTATCAAAACCTTGAAGTTTACAAGAAATTCGCCAGCTCTGGGAC
 CTTGGGACCCCTGCTGCTTGGATCCCTTCTGCTCCACCTGGTCCACCCAGCTGTGACGATGCGGGAGCTCAGG
 CGGGGCTCTGCTTTGGGATGGAAATGTGTTTTCTCCAAACTGTTTTTATAGCTCTGCTTGAAGGCTGGG
 AGATGAGTGGGTCTGATCTTTTCTCAGAGGTCTCCTACGATGATGGTGCATTCCGTTTCTATGATGATGAT
 TGCATTCAATAAACCAACAGCATCAAAAAA

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHGLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEGFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFCPSVISIQDVLCPVYDLNNAVAFIGMYQTMTKKAATVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEFPVDQGHRQKTLVSVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVLAIDRACPESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQYFWNIATIAVFYALPVVQLVITYQTVVNVVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRRALLRNDLCALECGIPKHFGFLFYAMGTALM
MEGLLSACYHVCPNYTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNATAFWIVFSIIHIIATLLLTQLYYMGRWKLDSGIFRRILHVLVYTDICIRQCSG
PLYVDRMVLVLMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALEFFFGGLSTWQKTPAESREHNRCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF
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Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCTTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTTGGGCGCTGGAGGGCCTGTCTGT
 ACC**ATGGT**CTCCCTGCCTGGCTGTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAATTTCCCTTTATACC
 TGACAAGTTGGCGCTGCCCGTGAAGGGGGCTGAAGGCCAGATCGTGCTGTGACGGGACTCA
 GGCAGGGCAACTGAGGGCCCATTTGCTATGGATCCAGATTTCTGGCTTCTCTGCTGGTGACCA
 GGCCTTGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGTACCCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCC
 CTTCTCTTCTTGTAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAATCGGATCTTCGAT
 TCCACATCTGTAGCCAGGCTCCAGCCAGCCTTCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
 CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCTATACCCGCACCACATGGCCAGGTACACTGGAAGTGGGGGTGATGT
 GCATATCACCTGAGAGGCCATCCCCGGGACCCCTTGAAGTGAATGCAGAGGGAAACCTCT
 ACGTGACCAGAGGACTGGACAGAGAAGCCAGGCTGAGTACTGCTCCAGGTGCGGGCTCAG
 AATTCCCATGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGAATGGATGAGAA
 TGACAACGTGCCTATCTGCGCTCCCGTGACCCACAGTACAGTCTCTGAGCTCAGTCAC
 CAGGTACTGAAGTACTACCTGTCTCAGCAGAGGATGCAGATGCCCCGGCTCCCCCAATTCC
 CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCCTTCCA
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCATCCGAGCAGGCCAGAA
 TCCTGCTTCTGTGTCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT
 GAAGTCGAAGTCGAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCCAGAT
 TGGGCCATAGAAGCTCCCTGAGGATGTGGAGCCCGGACTCTGGTGCCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCCGCCTTCCGCTCATGGATTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTTGCCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCCAAGTTGGACCAGGAGAGTACGAGGCCAGTGTCCCCATCAGTGCCCC
 AGCCGGCTCTTTCTCTGTACCATCCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCT
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATCTCCGGGAGGTTGCACCC
 GCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCCAGGA
 TACAGCCCTGACTCTTGCCCTGTGCCCTCCAATACCTCTGCACACCCCGCCAAAGACCATG
 GCTTGATGCTGAGTGACCCAGCAAGGACCCCGATCTGGCCAGTGGGACGGTCCCTACAGC
 TTCACCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCTCCAGACTCTCAATGGTTC
 CCATGCCTACCTCACCCTGGCCCTGCATTGGGTGGAGCCAGTGAACACATAATCCCCGTGG
 TGGTGAGGCACAAATGCCAGATGTGGCAGCTCTGGTTCGAGTGATCGTGTGCTCGCTGCAAC
 GTGGAGGGGACGTGCATGCGCAAGGTGGGCGCATGAAGGGCATGCCACGAAGCTGTCCGG
 AGTGGGCATCTTGTAGGCACCTGGTAGCAATAGGAATCTTCTCATCTCATTTTCAACCC
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCTGCCCTGAAGGCG
 ACTGTG**TGA**ATGGCCAGGACGCTTAGCTGGGAGCTTGGCCTTGGCTCCATCTGAGTCCC
 CTGGGAGAGAGAGCCAGCAACCAAGATCCAGAGGGGACAGGACAGATAGAAGCCCTCAT
 CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGCTGCAGAGCCTGGACACCAAC
 TTTATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTGTGCCCAATAATAAGCCCCA
 GAGAACTGGGCTGGGCCCTTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 132

MVPAWLWLLCVSPQALPKAQPAELSVVEVPENYGGNFPPLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
 HFSQAIYRRLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPMFQLEPRL
 GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEVSIESTWVSLEPIHLAE
 NLKVLYPHHMAQVHWGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN
 SHGEDYAAPLELHVLMVDENDNVPTICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
 VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTE
 GTFGLDWEPPDSGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGPGATATVTVLVERV
 MPPPKLDQESYEASVPISAPAGSFLLTIQPSDPISRTRLRFSLVNDSEGWLCIEKFSGEVHTA
 QSLQGAQPGDITYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHIIPVVVSHNAQMWQLLVRVIVCRCNV
 EGQCMRKVGRMKGMPTKLSAVGILVGTIVAIGIFLILIFTHWTMSRKKDPQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGGTGGATACTGTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTTAGTCAACTAGTAGTAATCAACAACCTGAAGCTCAATTTCTGGAAATCTCCCTCCTCT
 TCAATCGGCTGTGGATGTCTGGTCCCCTGTGCTAGTCTGCAGGCATTTAAATCCTTCTCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
 AGATGATGAATGCAACACATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG
 CTTACCATTTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCTTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTCTGTTGAAAACCGGCCGATGTATGTACTGAAGTT
 CAGCACTGGGAAAGCGGTGAGCGCGCCGCGCTTTGGCTGAATGCAGGCATCCATTTCCGAG
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACAGAGG
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTGCTGTGGCCAATCC
 TGATGGATATGTGTATATCAAACTCAAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC
 CTGGAAGCTCTGTCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAG
 GGAGCCAGCGACAACCTTGCTCCGAAGTGACCATGGACCCACGCCAATTCCGGAAGTGA
 GGTGAAATCAGTGGTAGATTTTCATCAAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
 ACAGCTACTCGCAGGTGCTGATGTATCCATATGGGTACTCAGTCAAAAGGCCCGAGATGCC
 GAGGAATCGACAAGGTGGCAGGGCTTGCGGCCAAAGCTCTGGCTCTGTGTGCGGGCATGA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGAGCAGTCTGAGTGG
 CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATCCCGGAGACTTCTGGC
 TTCTCTCCGACCTAACAGATCATCCCCACTGCGAGGAGACGTGGCTGGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTACTAGGCGCATGGCTCTGCTCTGTCTACATTTAT
 TTGTACCCACACGTGACGCACTGAGGCCATTGTTAAAGGAGCTTTTCTTACCTGTGTGAG
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCCCTCCAGCCAGCTCCCTGGAGT
 CGTGTGCTCTGGCGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCTCTG
 CTGTTTTTGTATGAGCCTTTGTCTGTTTCTCCTTCCACCCTCTGGCTGGGCGGCTGCACCT
 AGCATCACCCCTTCTCTGGGTGGCATGTCTCTCTACCTCATTTTTAGAACCAAGAACATC
 TGAGATGATTCTCTACCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT
 GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTTTAATTTT
 TCGCAGTCTTCTCTGGAAAATATTTTCTTTGAGCAGCAAACTCTGTAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCTCTCTGTTTTTTTTTTTTTTTGGAGACAGATTTTGTCTTTGTGTC
 CAGGCTGGAGTGTGATGGCTCGATCTGGCTCACCACAACCTCTGCCTCTGGGTCTCAAGCA
 ATTTCTCTGCTCAGCCTCTTGTAGTAGCTTGGTTTTATAGGCGCATGCCACCATGCTGGCTA
 ATTTTCTGTTTTTTAGTAGAGACAGGGTTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCCA
 ACCTCAGGTGATCTGCCCTCTTGGCCTCCACAGAGTGCTGGGATTTACAGGTGTGAGCCACTG
 TGCCGGGCCGCTCCCTCCTTTTTTAGGCCTGAATCAAAAGTAGAAGTCACTTTCCCTTAC
 TGTGTGAGAAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTATTTCAGTGTG
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATTTGCAGGATGGTGAATTAATCCCATCTGCTTAATGGGCTTACCTCTCT
 CTTTGCTTTTGAACCTACTTCAAAGATCTAGGCCTCATCTTACAGGTCTTAATCACTCATCT
 TGGCCTGGATAATCTCACTGCGCTGGCACATCCCATTTGTGCTGTGGTGTACTCTGTGTT
 TCTTTGCTGGTTTTG
 TCTGTCTATTTTGTATCTCGGACACAAGTTCCTAAGTAGAGCAAGAATTCATCAACAGCT
 GCCTCTGTTTTTCACTTCACTCAGCAGTACCATCTGTCTTTGTGTGTGTGTGTGTGTGTGT
 TTGTTTTTTTGTCTTTTACCAACATGTCTGTAATCTTAACTCTCTGCTTAGGATTTGTACA
 GCATCTGGTGTGTCTTATAAGCCAATAATATTCAATGTGAAAAAAAAAAAAAAAAA

MRWILFIGALIGSSICGQEKFFGDQVLRINRVNGDEISKLSQLVNSNNLKNLFWKSPSSFNR
PVDVLVPSVSLQAFKSFRLSQGLEAVTIEDLQALLDNEDDEMQHNEGQERSNNFNFGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSEFNRMVYLKfstGKGVRRPAVWLNAGIHSREWI
SQATAIWtARKIVSDYQRDPaITSILEKMDIFLLPVANPDGyVYTQTQNRlWRKtRSRNPgS
SCIGADPNRRWNASfAGKGASDNPcSEVYHGHPANSEVEVKSVDFDIQKHGNfKGfIDLHsY
SQLMlyPYGYSVKKAPDAEELDKVARLAALKASVSGTEYQVGTPTCTTyPASGSDIWAYD
NGIKFAFTfELRDtGTyGfLLPaQIIPtAEETWlGLKtIMEHVRDnTly

Signal peptide:
amino acids 1-16

[illegible]

FIGURE 136

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
 TPSQNIFFSPVSVSTSLAMLGLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
 SKDLTLKMGSAFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK
 VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTQVPMMHQKEQFAF
 GVDTELNCFVLQMDYKGDVAFFVLP SKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
 SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
 KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

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[illegible]

FIGURE 138

MKMQKGNVLLMFGLLHLEAATNSNETSTSTANTGSSVSSGASTATNSGSSVTSSGVSTATI
 SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFTASSGISIATNSESSTTSSGASTATNSE
 SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
 TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
 SNGAGTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTSS
 GASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
 NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEAST
 ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTMHTTSHSASTAV
 SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
 GPGGNHGHAPRRWSPNWFWRPVSIIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
 CCAGCAAT**ATGC**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
 CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG
 GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGC
 ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
 AAGGAGTTGGACAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
 CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC
 CAGGCTGGGAAGGAAGCAGAGAAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
 TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACAGCTGCTGAATGGC
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
 GGCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
 TGCCCT**TAA**ACTGGCATCCGGCCTTGTCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC
 ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGTTGTACTG
 GGATTGTGAATAAACTTGATACACCA

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FIGURE 140

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

[illegible]

FIGURE 142

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLSRDGRITLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLEEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFGNDPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFFSETGQEFFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFFPNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSACVFTMKDQVRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPGHLHTYDVLFLGTGDGRLHKAVSNGPRVHIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQ
QLATRPWIQDIEGASAKDLCSASSVSPSFVPTGEKPCQVQFQPNVTNLTACPLLSNLATR
LWLRNGAPVNASASCHVLPDGLLLVGTQQLGEFQCSWLEEGFQQLVASYCEPVVEDGVADQ
TDEGGSVPVIIISTSRVSAPAGGKASWGADRSYWKFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECASVHPKTCPVVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTESEKR
PLSIQDSFVEVSPVCPRRPRVRLGSEIRDSVV

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Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGCGCGCGCGCCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACC
 GCCAGCCAGCCGGAGGACCGGGGACGGGCGGGGACGGGAGCCCGGACTCGTCTGCGCGCGCCGTGTCGCGCGTGG
 TGC CGGCGCCGCGTCCCCGCGCGGACGCGGGAGGAGCCGCCCACTCGCGCCCGCGCGCTAGCGCGCGCG
 CGGGGACTGGTCCCTCTTAAAGGCGCAGGCCGCGCGCGCGGGGCGGGTGTGCGGAAACAAGCGCGCGCGGGGG
 CTTGCGGGCGGGCTCGGGGGCGCGATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGGCTCAGCGTGC
 CGCGGCTAGGCGGGCTGGCCCTCGTGGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCGCTGCGCGCGCGCGCG
 GCGCGCGCGCGCGCGCGCGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGGCTCAGCGTGC
 TGGCTCGGGCTCGTCTGGGCTTCGTGCTGGCTCGCGGCTCGTCTGCGCCGGGCTTCGAGCTGAAGCGAGCGGG
 GCGCGCGCGCGCGCGCGCGCGCGCGGGCTGCGGTCGCGGAGCGCGCGCGCTTCCAGCGCGCGCGCGCGCGCG
 GCGATGCGCGCGCGCGCGAGCTTGGCGCGCGCGCTCGGACCGAGATGGCGCGCGCGCGCAGCAGAACTTTCTCT
 TCGTGGGAGTCTAGTCTTCTTCAAGTAGGGTCTGACACATCTGTACCAATTCAGTAGTGCCACTACGGG
 GTGTGACGACTCTACCGCGCGCGCAGAAGACTCTTATGATGCTCAAGTACATGCACGCCACTACTTGGACA
 AGTATGAATGTTTATGAGAGCAGATGATGACGTGTACATCAAGAGACCCGTCTGGAAGACTTCTGAGGAGTT
 TGAACAGCAGCGAGCGCCCTCTTTCTGGCGCAGACGGCTGGCGCACACGGAAGAAATGGGAAACTGGCCCTGG
 ACCTTGGTGAGAACTTCTGCATGGGGGGGCGCTGGCGTATCATGAGCGCGGAGTCTCTCGGAAATGTCGCCCG
 ACATTGGTCAAGTGTCTCGGGAGATGTACACCACCCATGAGGACGTGGAGTGGGAAGTGTCTCGGAGGTTTG
 CAGGGGTCAAGTGTCTGTCTTATGAGATGCGGCAGCTTTTATGAGAATTACGAGCAGAACAAAGGGGT
 ACATTAGAGATTCTCCATACAGTAAATTCACCAAGCTATACATTACACCCCAACAAACCCACCTTACAGT
 ACAGGCTCCACAGCTACATGCTTGAGCCGCAAGATATCCGAGTCTCGCCATCGCACAAACAGCTGCGACGCGAAA
 TTGCTCTCATGAGCAATACAGCAACACAGAATACTCAATAAGAGGACCTCCAGCTGGGAATTCCTCCCTCTCTCA
 TGAGGTTTCAGCCCGCGCAGCGAGGAGGATCTTGGAAATGGGAGTTTCTGACTGAAATACTTGTATTCGCGAG
 TTGACGGCCAGCCCCCTCGAGAGGAAATGGACTCGGCCAGAGGGAAGCCTGGACGACATTTGATCAGGATCA
 TGGAGATGATCAATGACACCGCCAGACAGCAGGGCGCATATTGACTCAAAAGAGTCCAGTACGGTTCGCGCG
 GGGTGAAACCCATGTATGGGCTGAGTACATCTGGACCTGCTGCTCTGTCAAAAAGCAGAAAGGGAAGAAA
 TGAACGCTCCCTGTGAGGAGGACCGCGTATTTCAGCAGACTTTCAGCAAAATCAGTTTGTGGAGCATGAGGAG
 TGGATGCACAAGAGTTGGCCAGAGAAATCAATCAGGAATCTGGATCCTTGTCTTCTCAAACTCCCTGAAGA
 AGCTCGTCCCTTTAGCTCCCTGGGTGGAAGAGTGAGCAGAAAGAACCCAAAGATAAAAAGATAAATATCTGA
 TTCTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTATGGAAGAACTTTGAGAAGACGTGCTTATCCCCAATC
 AGAACGTCAAGCTCGTGGTTTGTCTTTCAATTCTGACTCCAAACCTGACAAGGCCAAACAGTTGAAGTATGA
 GAGATTACCGCATTAAGTACCCATAAGCGCGACATGAGATTTTGCTGTCTGGAAGAGCTTTTCAAGAGCCCTGG
 CCTGGAAGTAGGATCTCCAGATTTAAACAATGAATCTTTGCTCTTCTTCGCGACGTGACCTGCTGTGTTTACTA
 CAGAAATTCCTTCAGCGATGTCGAGCAAAATACAGTTCTGGGCGCAACAAATATATTTTCAATCATCTTCAGCCAGT
 ATGACCCAAAGATTGTTTATATGGGGAAGGTTCCAGTGACAAACATTTTGCTCTTACTCAGAAAACTGGCTTCT
 GGAGAACTATGGGTTTGGCATCACGTGATTATAAGGGAGATCTTGCCGAGTGGGTGGCTTTGATGTTTCA
 TCCAAGGCTGGGGGCTGGAGGATGGGACCTTTTCAACAAGGTTTTCAGGCGAGGTTTGAAGAGCTTTAGGAGCC
 AGGAAGTAGGAGTAGTCCAGCTCCACCATCTGTCTTTTGTGATCCCAATCTTGACCCCAACAGTACAAAGT
 GCTTGGGCTCCAAAGCATGACCTATGGTTCACCCAGCAGCTGGCTGAGATGTTGCTGGAAAAAATGATCCAA
 GTTACAGTAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTTAATGCTCCAGTTTGTGGAAGAACGTTTTT
 TAATATCTAATTTATTTTTCAAAAATTTTGTGATGATCAGTTTGTGAGTCCGTATACAGGATATATTTTAC
 AAGTGGTTTTCTTACATAGGACTCTTAAAGATTGAGCTTCTGAAACAAGAGGTGATCAGTGTGTCCTTTGAA
 CAGTCTCTTGTGCTGAACATTATGTAGCAGACCTGCTTAACTTGACTTGATGATGATGACAAACACTTT
 TTTAAAAAATGTTTCTTCTTGAGACCCCTTGCTCCAGTCTTATGGCAGAAACGTGAAACATTCCTGCAAGAT
 TATTGTGACAAACACTGTAACTCTGTAATGTTCTGTTGTGATTGTTAACTTCCAGCATCTACCTTTTGT
 GTTTTGTTTTTTTTTTTCAAATGCTTTTAAAGCCATTTCATGTTCCAGTTGTAAGATAGGAATAATGATAATA
 GCGTGTCTCATCATCTTTCACGAGAGCTTTCCAGAGTTGATCATTTCTCTCATGTACTCTGCTCAGCATGGC
 CAGTGAAGTTTTTGTGTTGTTTGTGTTGTTCTTTTTTGAAGCGGACTCTCACTCTGTACCAGCGCTGGAATG
 CAGTGGCGCAATCTTGCTCACTTAACTTCACTTCCCTGCTCAAGCAATTCCTCGCTTGGCTCCCGAGT
 AGCTGGGTTACAGGCACACACCCACCGCCAGNAGTGTTTTTGTATTTTAGTAGAGCGGGGTTTACCAT
 TCGAAGCCAGCTGGCCAGCTAGTTTTAAAGCAGGGGCGTGAAGAAGGCACAGTACGATCTGCTGCTTCTCG
 TGTGAGTCTATTGCGCCAAATAGACCTGGCATTAATTTTCAAGAGAGATTGGCATTTTCTCTTCTGACCCCT
 CTCTTTTAAAGGCTAAAATATTAATGTTTGAAGATGACAAGATGAATATATACATATATCTGATGTACAGACT
 GAAACATACACACATACCCCTAATCAAAACGTTGGGGAAGAAATGATTGTTTGTCTCTTCACTCTGTCTG
 TGTATTGTGGGTGGAGAGTGTTTTCATTCTTCTTACTGTTTGTGTTTATCTCTTGTATCTGAAATACCTTTAA
 TTTATTAAATATCTGTTGTTTCAGAGCTTGCCATTCTTGAGTACCTGTGATTAGTAGTATTATTATGTGTATCG
 GAGTGTGTTTAGTCTGTTTTATTTCGAGTAAACCGATCTCCAAGAGTTTCTTTTGGAAACGCTTTTTCCCTCC

FIGURE 143B

TTAATTTTATATTCCTTACTGTTTACTAAATATTAAGTGTTCTTTGACAATTTGGTGCTCATGTGTTTGGG
 GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAAGTTAAATTCAGATCAAATGTGCCTTAATAAATTTGTT
 TTCATTTAGATTTCAACAGTGATAGACTTGCCATTTTAATACAGTCATTGGAGGGCTGCGTATTTGTAAATAG
 CCTGATGCTCATTGGAAAAATAAACCACTGAACAATATTTTCTATTGTACTTTTCGAACCAATTTGTCTCATT
 ATTCCGTGTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAACTTAAACACGAAAAAA

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FIGURE 144

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTI PGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDVYIKGDRLNENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRVRRFAGVQCWVSYEMRQLFYENYEQNKKGYYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPMYGAEYILDLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVFPQLPGSKSEHKPEPKDKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVLVLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSTRALALEVGSSQ
FNNESELLFFCDVDLVFTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGDLVVRVGGFDVSIQGWGLEDDVLFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
 TTTCCGGCCTTGAGGTTCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
 ACGGACGACGCCT**ATGA**AGCCCTTAGTCCTTCTAGTTGCGCTTTTGCATGGCCTTCGTCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
 CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC
 TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGATCAAAATTTAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA
 ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
 ATTCTGGTCGATCAAACCAACAAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
 CAGGTGAACTGCGATAGAAAAACCCGAAGAGTTTGAAAGCACCCAGAGAGTTGGAATAAT
 GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC
 TAGATCTAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTTAT**TAA**ACAATAATATAAAATTTTAAACCTACTTGATATTCATAACAAAGCTGA
 TTTAAGCAAACGCATTTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT
 AAAAAATATTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGCATGTGTTATGAACA
 ATTTTCATATGCATAAAAACCTAATTTAAATAAAATTTTGGTTCAGGAAAAAA

FIGURE 146

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLNPISEETTTFPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEOPYIENEEPEPEPEPAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLEPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRTALLKVY
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Signal peptide:

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FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
 ACCTCCAAATCATCCATCCACCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACA
 GGAATATCC**ATG**GCTTTTGTGCTCATTITGGTCTCAGTTTCTACAGAGCTGGTGTGAGGACA
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTCTTTCCCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTCTCTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGAGAAGTGAAGTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGC
 TAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGTTTCACTGCCAGATTTTAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCTCTCATTCCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTCCCCCAGC
 CCACAGCCAAAGTGGAAAGGTCACAAAGGACAGGATTTGTCTTCAGACTCCAGAGCAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTGTGTTCCATCCACCTTGTGAGCAGAGTCAAGGTGGAATCCAAGGTATGATAGGAG
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGAAAAATCCA
 GGCGGAAGTGGAGTGGAGAAAGAACGACGGACAGGCAAGATTTGAGAGACGCCCGGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCGAAGCTCTGCGTTCTGTATCTGAAA
 ACTGTAACCCATAGAAAAAGTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
 AAAATGTAGGGTGGTATGTGGGAGTGTGTGCGGGATGACGTAGACAGGGGGGAAGAACATGTG
 ACTTTGTCTCCCAACATGGGTATTGGGTCTCAGACTGACAAACAGAACATTTGTATTTTAC
 ATTCATATCCCATTTTATCAGCCTCCCCCAGCACCCCTCTACACAGTAGGGGCTTCTCC
 TGGACTATGAGGGTGGGACCATCTCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC
 CTGCTGACATGTCACTTTGAAGGCTTGTGTAGACCCCTATATCCAGCATGCGATGTATGACGA
 GGAAAAGGGGACTCCCATATTTCATATGTCCAGTGTCTGGGGAT**TCAG**CACAGAGAAGACCCCTG
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGC
 CCCAGCTTCTCTCTCCGGAGCTGCGCACAGAGAGTCAAGCCCCCACTCTCTTTAGGGAGC
 TGAGGTCTTCTGCCCCTGAGCCCTGCAGCAGCGGCAGTCAAGCTTCCAGATGAGGGGGAT
 TGGCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGAGCGGAATAGACTCA
 CATTAGGTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAAGTCACAACTCC
 CAGGCTCCTCATTGTGCTAGTCACGGACAGTGATTCCTGCCTCACAGGTGAAGATTAAAGAGA
 CAACGAATGTGAATCATGCTTGCAGGTTTGAAGGACAGTGTGCTAATGATGTGTTTTTA
 TATTATACATTTTCCACCATAAACTCTGTTTGTCTTATCCACATTAATTTACTTTTCTCTA
 TACCAATACCCATGGAATAGTTATTGAACACTGCTTTGTGAGGCTCAAAGAATAAAGAG
 GAGGTAGGATTTTTCTACTGATTTCTATAAGCCAGCATTAACCTGATACCAAAACCAGGCAAG
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 TTCTAAATAAAAATTTAAACAAATTAACATAACAAATATTTAAAGATGATATATACTACT
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 CAGCACATTAATAAGTAAAAAGAAAACCATAAAAAAAAAAAAAA

FIGURE 148

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><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYGVCRDDVDRGKNNVTLS
PNNGYVWLRLTTEHLYFTFNPHFISLPPSTPPTTRVGVLFDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAGAGTTTGTGGGAACCCCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAGAAGACCTACAA
 TTACTATAGCACATTGTCAATTACAACGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA
 TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAATTTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
 GATCCTCACTCAGTTAAAAATAAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAAACTCTAGGTGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA
 GAACCCCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACCCATCACATGACTATGATATTCTT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAAACCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCAACAAG
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCT**TA**
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAAATGGAGAAGACTTGCAAACAGCTAGATTTGACTGATCTCAATAAAC
 TGTTTGCTTGATGCATGTATTTTTCTTCCAGCTCTGTTCGCGACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACCTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGAC
 TTGTTGACATAAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC
 AGCTCCTCTCATTTTCAGCAAAATATCCATTTTCAAGGTGCAGAACAAAGAGTGAAAGAAAATA
 TAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT
 GGAATATTAGAAATGATCATATTTATTGAAAGGTCAAGCAAGACAGCAGAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAACAAAGTTAAGGAAGTCCAGAAAGAACCCAGATATA
 TCCTTATTTTCATTTCCAAACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG
 ACCTATAATAATTATACAAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAATCACCCA

FIGURE 150

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVFYTNVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHRLQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWLIVLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

```

Transmembrane domain:

amino acids 21-40 (type II)

1-10
 11-20
 21-30
 31-40
 41-50
 51-60
 61-70
 71-80
 81-90
 91-100
 101-110
 111-120
 121-130
 131-140
 141-150
 151-160
 161-170
 171-180
 181-190
 191-200
 201-210
 211-220
 221-230
 231-240
 241-250
 251-260
 261-270
 271-280
 281-290
 291-300
 301-310
 311-320
 321-330
 331-340
 341-350
 351-360
 361-370
 371-380
 381-390
 391-400
 401-410
 411-420
 421-430
 431-440
 441-450
 451-460
 461-470
 471-480
 481-490
 491-500

FIGURE 151

CTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCC**ATGCT**GGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
 CGTGACCTTCTTGGTTCACAGAGCTCAGCCCTTGCCCCCTCAAGACTTTGAAGAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCTTTGCCGGCTGTCCCTGCGACTACGACCACTGC
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCTGCCTGTGCCC
 AGGACTCTCCAGCCCCGCCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCGGTCTCCTCACTACTGG
 CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGGCCCCGCTGAACGCTACGTTCCG
 CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATGTCGTTTGCCTAGTGCGCCGCTA
 ACGAGGCCGGGGCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
 CCTGCCTTCGGGCCTTGACAGCCGCTTGCGGTGCCGCCCAACCCCGCACTCTGGTCCACGC
 GGCCGTGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCGCGATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCTC**TGA**
 AAGGGGCTGGGGGCTCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCG
 GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
 GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTTAGTCCGGTACTT
 GGCGCTTTGTTTCTTGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCAATTTTTTTTTTA
 AGCGGCCAGATAATAATAATGTAACTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAPQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPLGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLDWGSEA
AQKGPPLNATVRRRELKGLKPGGIYVVCVVAANEAGASRVPAAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAAGVGTALALLSCAALVWHFCLDRWGCPRRAAARAAGAL
```

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAACGCTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCCGATGAGCCCCCGCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACC
 CCCAGCGCCGACGATCGCTGCCGTTTGCCCTTGGGAGTAGGATGTGGTGAAGGATGGGG
 TTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCCGTGCTGCT
 CTACGCCCTCAATCTGCTCTTTGGTTAATGTCCATCAGTGTGTGGCAGTTTCTGCTTGGA
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC
 ATTTGACTTACTTTCCTGTGGTTTCATCCGGTCATGATTGCTGTTTGTGTTTCTTATCAT
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAGAAATCTGTTGCTTCTTGCATGGTACT
 TTGGAAGTTTGTCTGTCATTTCTGTGTAGAACTGGCTTGCGGCTTTGGACATATGAACAG
 GAACCTTATGGTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTCAGAGAGAGTTTAACT
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCAGAT
 TCCTGCTGTGTTAGAGAAATCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTGTGGGAAGAAATGTATTCCTTTTGGAGGAACCAACACTGC
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAATCCTGGCCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTC
 CTTGAAGAATGACAACCTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCC
 TGTCAAGAATCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGAG
 GAGTTATAAAGAAATGTCACAGAAGAAACCAAACTTGTTTTATTGGACTTGTGAATT
 TTTGAGTACATACTATGTGTTTTCAGAAATATGTAGAAATAAAAAATGTTGCCATAAAATAAGA
 CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTT
 CGCATCCATGCAACAGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTT
 CTACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATATATATCAGAAAACTTTC
 AATATTGGTGACTACCTAAATGTGATTTTGTCTGGTTACTAAAATATTCTTACCACTTAAAA
 GAGCAAGCTAACACATTTGTCTTAAGCTGATCAGGGATTTTTTGATATAAGCTGTGTTAAAA
 TCTGTATAAATCAGTCGATTTTCACTTCTGATAATGTTAAGAAATAACCATATGAAAGGAAA
 ATTTGTCTGTATAGCATCATTATTTTTAGCCTTTCTCTGTTAATAAAGCTTTACTATTCTGT
 CCTGGGCTTATATTACACATATACTGTTATTTAAATACTTAACCACTAATTTGAAAATTA
 CAGTGTGATACATAGGAATCATTATTTCAGAAATGTAGTCTGGTCTTTAGGAAGTATTAATA
 GAAAATTTGCACATAACTTAGTTGATTTCAGAAAGGACTTGTATGCTGTTTTCTCCCAATG
 AAGACTCTTTTGCACATAAACTTTTAAAGAGCTTATCTTTGCGCTTCTCCAAACAAGAA
 GCAATAGTCTCAAGTCAATATAAATTTACAGAAATAGTGTCTTTTCTCCAGAAAAAT
 GCTTGTGAGAATCATTAACATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTA
 ATATACTGTGGCAATTTACACAGATTATAAATTTTTTCAAGAGTATAGTATATTTATTT
 GAAATGGGAAAAGTGATTTTACTGTATTTTGTGATTTTGTGTTTATTTCTCAGAAATAGGAA
 AGAAAATTAATGTGTCATAAATATTTTCTAGAGAGTAA

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
```

```
><subunit 1 of 1, 305 aa, 1 stop
```

```
><MW: 35383, pI: 5.99, NX(S/T): 0
```

```
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVWYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSLDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCCTGCC
 TGCACTCGGGCCTCCTCCAGCCAGTGTGTACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCAGAGGCCAGC**ATG**TTACAGGATCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGG
 TGATTCTGGATAAATACTACTTCCCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCAGAGGCCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA
 TGTGTTGAAATCACAGAAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCT
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGACCTGAAGACCCCCCGT
 GTGGTGGTGGGGAGGAGGCCCTCTGTGGATTCTTGGCCTTGGCAGGTGAGTCCAGTACGA
 CAAACAGCACGCTCTGTGGAGGGAGCATCTTGACCCCCACTGGGTCTCACGGCAGCCCACT
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAA
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTCACTTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA
 TGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
 GGTCAATTGACAGCACCGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTACCAGAGAAGA
 TGATGTGTGACGCATCCCCGAAGGGGGTGTGGACACCTGCCAGGCTGACAGTGGTGGGCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
 GGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCTCTG
 CCGTGCCACCTGGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCC
 CTCGCCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACCC
 TCGAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGTCTCC
 AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
 GGAACCTTTCCACACTACTGAATGGAAGCAGGCTGTCTGTGTAAGCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCACATCCCCAGCCTA
 CTAGAGCAAGAAACAGTTGTAATATAAAATGCATGCCCCACTGTGTTGGTATGACTACCGTT
 ACCTACTGTTGTATTGTTATTACAGCTATGGCCACTATTATTAAGAGCTGTGTAACATCT
 CTGGCAAAAAAAAAA

FIGURE 156

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSQQPLNSLDVKPLRKPRIPMETFRKVGIPITIIALLSLASIIIVVVLKIVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNNSGPGCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWFWQVSIQYDKQHVCSSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAPIPE
GGVDTCCQGDGGPLMYQSDQWHVVGIVSWGYCGGPGSTPGVYTKVSAYLNWIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGACGCGCATCCCCAGGCTCCAG
AGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCAGCCCTGGGCCTGGACCCCTGGAGCCTCCTGGGCC
TTTTCTCTTCCAACCTGCTTCACTGCTGCTGCCAGCAGCACCGCGGGGGAGGCGGGCAGGGGCCCATGCCCA
GGGTGAGATACTATGCAAGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA
CTCTGCTCCTGAGTGGTGTGGAATACTCTCTACGTGGGGGCTCGAGAAGCCATCTGTGGCCTTGGATATCCAGG
ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCC"TTA
AGAAGAAGAGCAATGAGACACAGTGTTTCAACTTCATCCGTGTCTCGGTTTCTTACAATGTACCCCATCTCTACA
CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCCCATCTCGG
AGGACAAAGTTCATGGAGGGAAGGCCAAAGCCCTTTGACCCCGCTCACAGCATACGGCTGTCTTGGTGAGTG
GGATGCTCTATTCTGGTACTATGAACAACCTTCTGGGCAGTGAGCCCATCTGATGCGCAGCTGGGATCCAGC
CTGTCTCTCAAGACCGACAACCTTCTCGCTGGCTGCATCATGACGCTCCTTTTGGCAGCCATCCCTTCGAGCC
AGGTCGTCTACTTCTTCTTCGAGGAGACGCCAGCGAGTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG
CTAGAGTCTGCAAGATGACGTGGCGGGCGAAAGCTGCTGCAGAAGAAGTGGACCACTTCTCTGAAGGCCCAGC
TGCTCTGCACCCAGCGCGGGGCACCTGCCCTTCAACGCTCATCCGCCACGCGCTGCTTCCCGCGGATTCTCCCA
CAGCTCCCACATCTACGCAGTCTTACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT
TCTCTCTCTTGGACATGAACTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTA
CTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCAGTTGCTCAGTGGGCCCTCCTCTGTATAAGGCCCTGACCT
TCATGAAGGACCAITTTCTGTATGATGACGAAGTGTGGGGACGCCCTGCTGGTGAATCTGGCGTGGAGTATA
CAGCGCTTCGAGTGGAGACGCCAGGGCCTTGATGGGCACAGCCATCTTGTGATGTACCTGGGAAGCAACCCAG
GGTCGCTCCACAAGCTGTGGTAAAGTGGGGACAGCAGTGTCTATCTGGTGAAGAGATTGAGTGTTCCTGACC
CTGAACTGTTCGCAACCTGCAGCTGGCCCCACCCAGGGTGCAGTGTGTAGGCTTCTCAGGAGGTGTCTGGA
GGGTGCCCCGAGGCCAATGTAGTGTCTATGAGAGCTGTGTGAGCTGTGCTTGGCCCCGAGCCCCCACTGTGCCT
GGGACCTGAGTCCCGAACCTGTGGCTCCTGTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACATGGAGCGGG
GGAAACCCAGAGTGGGCATGTGCCAGTGGCCCATGAGCAGGAGCCTTCGGCCTCAGAGCGCCCGCAATCATT
AAGAACTCTGGCTGTCCCCAACTCCATCTGAGCTCCCTGCCCCACCTGTGAGCCTTGGCCTCTTATTATT
GGAGTCATGCCCCAGCAGCAGTCCAGAAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGTGTGATGTCAGG
ATTGAGTTGGGGGTCTTACACAGCTGTGGCACTGAGAATGGCTTTCTACACCTGTGATCTCTGATCTGGGTGG
ACAGCCAGGACCAGACCTTGGCCCTGGATCCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA
CCAGGGTCAGTGGTGGGCGGCCCTGGCTGCCAGCAGTCTACTGGCCCCACTTTGTCTACTGTCACTGTCTCT
TTGCCTTAGTGCTTTTCAAGAGCCCTCATCATCTCTGTGGCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGG
TTCAAGGCTGTGAGACCTTGGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAG
AATGCAAGGACTCTGCGCACTGATGTGACAGCTGACAACAACCTGCTAGGCATGATGAGCTTAAACTCTAGGCA
CAGGCCGGGCTGCGGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCCAAGCAGCCCTGACTAGGATGACAG
CAGCACAAGAACCACTTTCTCCCTGAGAGGAGCTTCTGTACTCTGCACTCACTGATGACACTCAGCAGGGTG
ATGCACAGCAGTCTGCTTCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTTAAACAGGGTGGGGCTAC
CCCCAGACTGCTCCTACAGTGTATGTAAGAACCTGGAGAGGATCGTCACTTCTGGCATTCAGGACCCCTC
CAGAAACACAGTGTTCAGAGAGCCCTAAAAAACCTGCCTGTCCAGGACCCCTATGGTAATGAACACCAACATC
TAAACAAATCATATGCTAAATGCACTCTGGAACTCCACTCTGAAGCTGCGCTTTGGACACCAACACTCCCT
TCTCCAGGGTCATGACAGGATCTGTCTCCTCTGCTTCCCTTACAGTCTGACACCGCTGACTCCAGGAAGTGC
TTTCTGAAAGTCTGACCACCTTTCTTCTGTCTCAGTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAAATGG
CAGGGTAACTGAGCCCTTCTTCACTCCTTTACCTTAGCTGACCCCTTCACTCTTCCCTCTTCTTCTTCTTGT
TTTGGGATTAGAAAACCTGCTGTGCAGAGCTGTTTATTTTATTAAAAATATAAGGCTTAAAAAA

FIGURE 158

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGPMRVRYYAGDERRALSFFHQKGLQ
DFTDLLLSGDNLTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFILMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLSHKAVVSGDSSAHLVEEIQLFPDPEPVRLNLQLAFTQGAVFVGFSGGVVRVPRAN
CSVYESCVDCLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGFAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFAVLVSGALIILVASPLRALRARGKVQCETLRPGKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTTAGAAG
 TGAGC**ATGG**GCTGGGCGAGCGAGTGCTTCTTCTAGTGGGCTTCCCTTCTCCCTGGGGTCTCGCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCCACCATGCTTAACCACAAAAGAG
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGTATTTCTTCTGGAAGAACTTTAGG
 TGGCAGAGGAAAATTTGAAAACCTTATTAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
 ATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAAATGAGAACTTCGACATGGTGATA
 GTTGAAACTTTTGACTACTGTCTTCTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC
 CATTCTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTT
 CAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTCTG
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAAACACCATCAA
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
 GGTTCAATAACTCTGACTTTGCCTTTGATTTTGGCTCGACCTGCTTCCCAACACTGTTTAT
 GTTGAGGGCTTGATGAAAAACCTATTAACACAGTACCACAAGACTTGGAGAACTTCATTGC
 CAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTCAGA
 ATCCGGAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCAGTGTTCTCATTTGGCCCAAAGATGTCCACCTGGCTGCAAAATGTGAAAATTTGGGA
 CTGGCTTCTCAGAGTGACCTCCTGGCTCACCAAGCATCCGCTGTGTTGTCAACCACGGCG
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
 GGAGACAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTACAGTT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGCGCAGTGGCTGCCAGTGTCTCTGCGCTCCCACCCGCTCAGCCCCACACAG
 CGGCTGGTGGGCTGGATTGACCACGTCCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGC
 TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT
 GGGCCGAGAAGGTGAAGGAGACA**TAA**GGCCAGGTGCAGCCTTGGCGGGTCTGTTTGGTGG
 GCGATGTCAACATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC
 TAATTTTGTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCTCT
 CTTGTCTCCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTGG
 GACCACTGACCTCAGATTTCCAGCCTTAAAAATCCACCTTCTCTCTATGCGCCTCTCCGAA
 TCACACCTTGACTCTTCCAGCCTCCATGTCAGACCTAGTCAGCTCTCTCACTCCTCGCCCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACCTTGCATATCTTTCACTTTCTGTTT
 TGTTCTCCACATATTTCTCTTCAATGCTCAGGAAGCTGCCCTGTGCTTGAGAGTTCAAGGC
 CGGACACAGGCTCACAGGTCTCCACATTTGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCT
 TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACA
 CGCTTATCTCTCCCAACCTCACTAA

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FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKRGP
 FMPDPFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
 LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPVFAILSTSFGSLEFGLPIPLSYVPV
 FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAEWLF
 INSDFAFDFAFPLLPNTVYVVGGLMEKPIKFPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
 EIFKEMNNAFAHLPQGVWKQCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
 NSIMEAIIQHGVPVMGIPLFGDQFENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
 SAAVAASVILRSHPSPQRLVGVWIDHVLQGTGGATHLKPYVFQQPWHEQYLFDFVFFLLGLT
 LGTLWLCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
GCCTCTGGCATATGCACACACTCACACATTTCTGTACACCCGTCACACACACATACATGTT
CTCCATCCCCCAGGTCACAGCCCTAGTGCTGTCCCATCCAGCAGGGCTACCCCTGAAGCTCT
GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCAAAGCCCA
ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
GGGAGGCAGGACAGAGTGGGACACAGGTATGGAGAGGGGGTTCAGCGAGCCCTAGAGAGGGC
AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAACAAGAAGAGGGGCAGA
AGACCGGGGCACTTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCCACTGGC
TACCAGTCCCCACACAGTCCCGGGCTGCCCTTGGTTCTGTTGCTTCTGGCCCTGGGGGCC
GGGTGGGCCCAGGAGGGGTCAGAGCCCGTCTGCTGGAGGGGGAGTGCCCTGGTGGTCTGTGA
GCCTGGCCGAGCTGCTGCAGGGGGGCCGGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
GAGTGGCATTGTCTCGGTCGAGCCAGCCACCATTGAGCCAGCAGGGGAAACCGCAATGGC
ACCAGTGGGGCCATCTACTTCGACAGGTCCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
CTCTGGCTCCTTCGTAGCCCTGTCCGGGGTGCTACAGCTTCGGTTCCATGTGGTGAAG
TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCTCAGCC
TTTGCCAATGATCCTGACGTGACCGGGGAGGCAGCCACGCTCTGTGCTACTGCCCTTGA
CCCTGGGGACCGAGTGCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAATACT
CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCTGAGGACC AAGTCTTTCAAGCACAAGAAT
CCAGCCCCTGACAACCTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAG
ACTCCCTCTGGCTCCTATCCACCTCTTTGCATGGGACCCGTGTGCCAAACACCCAAGTTTAA
GAGAAAGATAGAGCTGTGGCATCTCCAGACCAGGCCCTTCCACCCACCCACCCCACTTACC
CTCCAGCCACCTGCTGCATCTGTTCTGCTGTCAGCCCTAGGATCAGGCAAGGTTTGGA
AGAAGGAAGATCTGCACACTTTTGGCGCTCTGCTCTCCGGTTCCTCCACCCAGCTTCCT
GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCAG
ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCCTGTAGGAAAGCCAGCATCAGGGATC
TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGTTGGGAGGCTCAGCCAC
AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGTGATTTG
TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGACAGCCAGCAGGTAGCAATCCT
GGCTGTCCTTCTATGCTGGATCCCAGATGGAAGTCTGGCCCTTACCTCCCCACCTGAGATTG
GGTGAGTGTGTTTGTCTGCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
ACCATGGAACATCATGATAACCATGCATCCTCTGCTTGGCCACCTCCTGAAACTGCTCCAC
CTTTGAAGTTTGAACCTTAGTCCCTCCACACTCTGACTGCTGCCCTCTCTCTCCAGCTCTC
TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCACTATCTCTCTTTCTCCTGAT
CTGTGCTGTCTTATCTCTCCTCTAGGCTTCCTATTACCTGGGATTCATGATTCACTCCCT
GACACCTCTCCTGCCAGTATGCTAAACCTCCCTCTCTCTTTCTTATCCGCTGTCCCAT
GGCCCAGCCTGGATGAATCTATCAATAAAACAAGTAGAGAATGGTGGTCACTGAGACACTAT
AGAACTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTACAGGTACAAGTAGGTA
GTTGACAGGAAAAATAATATCAAACCTGTATACATAAAATAAAAA

FIGURE 163

[illegible]

FIGURE 164

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVDWNTPKKGGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPIITIPKLEHPTQQDIDLYHTMYEALVKLFDK
HKTKFGLPETEVLEVN

```

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

GGGCGCGGGGATGGGGGCGGGGGCGCGGCGCGCTCGCTGAGGCCCGACGACGAGGGCGGGCGGGGCCCA
 GGGCCGAGGAGCGCGCGCCAGAGCGGGGCGCGGAGGCGACGCCGGGACGCCCGCGCGAGCAGGCTGGCG
 CGGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCTTGGGA
 CGGCTGTCTCAGCGAGGGGCGGTGCACCCGCTCTTGAGCAGCGCCATGGGCGCTGCTGGCCCTTCTGAAGACCCA
 GTCTCGTGTGCACCTGCTGGCTTGTCTTCTCGTGGTGAAGTGGTGGTCACTCAACTGCTGCAGCTGTGCAC
 GCTGGCGCTGTGGCGGTGAGCAAGCAGCTCTACCGCGCCTCAACTGCCGCTCGCTACTCACTCTGGAGCCA
 ACTGGTCACTGCTGGAGTGGTGGTCTGCACGGAGTGTACTCTGTTACGGAGCAGGCCACGGTAGAGCGCTT
 TGGGAAGGAGCACGAGTCATCATCTCAACCACAACCTTCGAGATCGACTTCCCTGTGGTGGACCATGTGTGA
 GCGCTTCGGAGTGTGGGGAGCTCCAAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGGCTGGAC
 GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGACCGGGACACCTGGTTCGAAGGGCTGAG
 GCGCTGTGCGACTACCCGAGTACATGTGGTTTCTCTGTACTGCGAGGGGACGCGCTTCAGGGAGACCAAGCA
 CCGCTTAGCATGGAGTGGCGGTGCTAAGGGGCTTCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG
 CTTCAACCACCGAGTCAAGTGCCTCCGGGGGACAGTCGAGCTGTCTATGATGTAACCTGAACCTCAGAGGAAA
 CAAGAACCCGCTCCCTGCTGGGGATCTCTACGGGAAGTACGAGGCGGACATGTGCTGAGGAGATTTCCTCT
 GGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAATGTACCGAGAGAAGGACGCGCTCCA
 GGAGATATATAATCAGAAGGGCATGTTCCAGGGGAGCAGTTAAGCTGCCCGAGGGCGGTGGACCTTCTGAA
 CTTCTGTCTCTGGGCGACCATTTCTCTGTCTCCCTCTTCAAGTTTGTCTTGGGCGCTTTTGCAGCGGATCACT
 TCTGCTGATCTTCTGGAGATTGTGGGGTGTGGGAGCAGCTTCTTGTGAGTTCGACACCTGATAGAGAGATTCGCT
 TGAACCTGGGAGTGGAGATTGCACTGAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
 CAGTCTCAAAAAAAAAAAAAACAAAAACCCAGAAATTTCTGGAGTGAACCTGTGTAGTTACTGACATGAAAA
 ATTCACTAGAGGCTGAACAGCAGATTGTAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAAT
 TTTCAAGCTAATGAAAAAGATGAAGGAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA
 CATATGCATGATGAGAGTCCCGAAGGAGAGAGAGAAAGGTCAGAAAGATGGCCCAAGCTGATGAAAAACA
 GTAACCTACCACTCAGGAAGCTCAGTGAATCCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTCA
 ATCAAGATGTCAAATGACAAAGATCTTGAAGCAGCAAGAGATGAGCAACTTATCTTGTCAAAGGATCTTGA
 ATCAGATTAAACAGCTCATTTCTCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
 AACCTTCAACTGTAATTTATGGAACTTTGAGTCTTAGATGGCTCTGACCTCTTGTCTTCAGGAGCAGTTTTC
 ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTGAACCTGTAGGAAGGCTGTCTTTAGGCCGGGACAGTGGC
 TTACACCTGTAATCCAGCAGCTTGGGAGGCCAGAGCGGTGGATCATTTGGGTGAGGCTGATCTCAAACTCT
 GAGTTTCAGGTGATCTGCCGCCCTCAGCCTCCCAAAGTGTGTGATTGCAGGCGTGAGCCACTGCGCTGGCCGA
 ATTTCTTTTAAAGCTGAATGATGGGGGCCAGGCACGATGGCTGACCTCTGACCTTCTGTCTTCCAGGCTGGATTGA
 AACATGCACCACTACCTGCCTGGCTAATTTTGTATTTTATGATAGAGACGTGTTAGCCAGGCTGGTCTCGATCTCCT
 GACCTCAAGTGACCACTGCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCTGGCCTTGA
 GCACTCTGTGATGTCTTATGGCCATTTGTATATCTTCTATCTCTTGGGGAAGTGTCTGTTCAAGTCTTGT
 CTTTCTTTTAAATTTTATTTATTTATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
 CAGTGGCAGCAGTCTTGGCTACTGCAGCCTCGACCTCTGGGCTGCAGTATCTCCACCTCAGCCTCCCTTGT
 AGCTGTATTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTACCATGA
 TGGCCAGGCTGGTCTGAACCTCCTGAGCTCAAGTGTATGCGCTGCTTCAAGCTCCCAAAGTGTGGGATTACAGA
 CATGAGCCACTGCACCTGCCAACTCCCAAATTCACACACACACAAAAACCACTGATTCAAAATGGGCA
 GAGGGCGCGGTGTGGCCCCAACTACAGGGAGACTGAAGTGGGAGATCGCTTGGGCATGAGAAGTCGAGGCTG
 CAGTGAAGTCGAGTTGTGCGACTGCATTCAGCCTGGACAACAGAGTGAACCTGTCTC

FIGURE 166

```
></usr/segdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTKQFVLHLLVGFEVSVGLVINQVQLCTLALWVPVSKQLYRRLNCRSLAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCRKRWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLILITFLGFVGAASFGVRRLLIGESLEPGRWRLQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA
 GCCACCAGGCATATTTCATCTTTGTGTGTGTTTTCTTTTGTCTTTAGCACTGGGGCACTTCTT
 GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTTGTGGGGTTGGTGGCAGGCAGGCCG
 GCTTACGCCGTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
 GATAGCTGGGGTCTGAGACCTGCTTCCCTCAGTAAAATTCTCTGGGATCTGCCTATACCTTCTT
 TTCTCTAACCTGGCATACCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGT
 ACATGTGGTGTCTCTTGTCTGTTCTCTGTAATGTGGTATGCCATGGGGTCTTGCACAAGCCT
 TTCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCTACTTAATATGTAGTC
 ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTGTGTTAATGCTCTCATAAGACCATTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA
 TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
 TGCCTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT
 CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTACCA
 GATGGTGTAGGGCCAGCATTGTAAATTACACGTTGACTGTGCTTGTGAATTATCTGGGGA
 TGCAGGTCTTGATTGAGTGTAGGCCAGGTTGGGCATCTCTAACAACTCCACGATGATGCTGA
 TGCTGGTCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
 TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCCACATGGTGAACCCCATCTGTACTAAAAATACACAAATTAGCTG
 GGCATGGTGGCACATGCCTGTAGTCCAGCTACTTTGGGAGGCTGAAGCAAGAGAATCGCTTG
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAA

FIGURE 168

```
></usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSIQCPGAATRIHILCVCFSFALALGHFLLISLVGKGLSLSCGVGGRRQAGRLRLIRPWVRR
EGKINFYFTNGDSWGLRPASSVKFLGSAYTFFSLTWHHTLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGOLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
TTATAGGTGAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTCAGCAACTAAAAAGCCAC
AGGAGTTGAACCTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCTACTCTACCTAC
ATTAATACTGTTTTTTGTCTCTTGTAAGTACCTTTACCTTCCTAACACAGAGGATCTGT
CACTGTGGCTCTGGCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC
ACCGTCCCTCGAAGCCGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAAGTAGCTGAGCCTCTTGGA
GCTGCGGCTTTCAAGGTGGGCTTGCCCTGGCGTAGAAGGGAT**TGA**CAAGCCGAAGATTT
CATAGCGATGGCTCCCACTGCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT
CTAACCTTTTCATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACCTCTGTCCCAAGG
AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
TATGTGACAGGACTTGCACTTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
GGGAAGGAACCTTGTCCAAATATGGGTGAGAAAGATGGAGGTGTTGGGTTATCACAAGGC
ATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCAGTACCAGCTGCTG
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCCATCACCAG
CCAGGGGCAGCCGCTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCCCCTCTTCCCTC
TGAGAGGCCCTCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
GCTCAGTGTTGGCCAGGAGGTGAGCAAGCCTGAGAGCTGATCAGAAGGGCCTGTGTGCG
AACACGGAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCAGGCAAGGACTGTGTGGCT
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAA
TCCAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCGGGGTGTGGTGGCCTGTAATG
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTG
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAATAGCCAGGCATGGTGGT
GTGTGCCTGTATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
AAAAATAAAAAAGAAATTATGGTTATTGTAA

FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
```

```
><subunit 1 of 1, 109 aa, 1 stop
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><MW: 11822, pI: 8.63, NX(S/T): 0
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```
MLWWLVLLLLPTLKSVCFLVTSLYLPNTEDLSLWLWPKPDLSHSGTRTEVSTHTVPSKPGTA  
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
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Signal peptide:

amino acids 1-15

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FIGURE 171

GCGGGCCCGCAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
 CCGCCGCCTCCTGCCCGGCC**ATGA**CCAGCCGGTGCCCCGGCTCTCCGTGCCCCCGCGCT
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCCTCTTCTGGGGAGGCGGT
 GCCCCCATGGCGAGGCCGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCTGTGG
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
 CCTGGAGCAGCCGCAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGCCAACC
 TGGCGCGGCTCATCCAGGCCAAGAAGCGCTGGACCTGGGCACCTTCACGGGCTACTCGCC
 CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
 GCCCCGGAGCTGGGACGGCCCTGTGGAGGCGAGGCCGAGCGGAGCACAAAGATCGACCTCC
 GGCTGAAGCCCGCCTTGAGAGCCCTGGACGAGCTGCTGGCGGCGGGCAGGCCGGCACCTTC
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCCTACTACGAGCGCTGCCTGCA
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCTGTGGCGCGGGAAGGTGCTGC
 AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
 GACGTCAGGCTCTACATCAGCCTCCTGCCCTGGCGGATGGACTCACCTTGCCCTTCAAGAT
CTAGGGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
 CCTGAGTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

FIGURE 172

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQFPVRLSVFAALALGSAALGAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRs
MREHPALRSRLRLTLEQPGQDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPELGRPLWRQAEAEHKIDRLKPALETLDELLAAGEAGTFDVAVVDA
DKENCsAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

CCGCGCGCCGAGCCGCTACCGCCGCTGCAGCCGCTTTCCGCGGCCCTGGGCTCTCGCCGTCA
 GG**ATG**CCACACGCCTTCAAGCCCGGGGACTTGGTGTTTCGCTAAGATGAAGGGCTACCCCTCAC
 TGGCCTGCCAGGATCGACGACATCGCGGATGGCGCGTGAAGCCCCCACCACCAAGTACCC
 CATCTTTTTCTTTGGCACACACGAAACAGCCTTCTCTGGGACCCAGGACCTGTTCCCTACG
 ACAAATGTAAAGACAAGTACGGGAAGCCCCAACAGAGGAAAGGCTTCAATGAAGGGCTGTGG
 GAGATCCAGAACACCCCCACGCCAGCTACAGCGCCCTCCGCCATGAGCTCCTCCGACAG
 CGAGGCCCCCGAGGCCAACCCCCGCCAGCGAGTGACGCTGACGAGGACGATGAGGACCCGG
 GGGTCATGGCCGTACAGCGGTAACCGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA
 GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCTTGCCTAAAGATGTC
 GTCTCTGAAACGAGCCCCGAAAGGCCTCCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG
 AAGAGGAAACTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACGAGGACTTCACACCT
 GAGAAGAAAGCAGCGGTCCGGCGCCACGGAGGGGCCCTCTGGGGGACGGAAAAAAAGAA
 GCGCCGCTCAGCCTCCGACTCCGACTCCAAGGCCGATTCGGACGGGGCCAGCCTGAGCCGG
 TGGCCATGGCGCGGTTCGGCTCCTCCTCCTCCTCCTCCTCCTCCTCCGACTCCGATGTG
 TCTGTGAAGAAGCCTCCGAGGGGAGGAAGCCAGCGGAGAAGCCTCTCCGAAGCCGCGAGG
 GCGGAAACCGAAGCCTGAACGGCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG
 TGGACCGCATCAGTGAGTGGAAGCGCGGGACGAGGCGCGGAGGCGGAGCTGGAGGCCCGG
 CGGCGCGGAGAGCAGGAGGAGGAGCTGCGGCCCTGCGGGACGAGGAGAAGGAGGAGAAGGA
 GCGGAGGCGGAGCGGGCCAGCCGCGGGAGGCTGAGCGGGGACGCGGCGGACGAGCGGGG
 ACGAGCTCAGGGAGGACGATGAGCCCGTCAAGAAGCGGGGACGCAAGGGCCGGGGCCGGGGT
 CCCCCGTCTCCTCTGACTCCGAGCCCGAGGCCGAGCTGGAGAGAGAGGCCAAGAAATCAGC
 GAAGAAGCCGAGTCTCAAGCACAGAGCCCGCAGGAAACCTGGCCAGAAGGAGAAGAGAG
 TCGCGCCCGAGGAGAAGCAACAGCCAAGCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCC
 GAGGGCTTCTCGATGGACAGGAAGGTAGAGAAGAAGAAAGCCCTCCGTGGAGGAGAAGCT
 GCAGAAGCTGCACAGTGAGATCAAGTTGCCCTAAAGGTGCGACAGCCCGACGCTGAAGAGGT
 GCCTGAATGCCCTAGAGGAGCTGGGAACCTGCAAGTGACCTCTCAGATCCTCCAGAAGAAC
 ACAGACGTGGTGCCACCTTGAAGAAGATTGCGCGTTACAAGCGCAAGGACGTAATGGA
 GAAGGCAGCAGAAGTCTATACCGGCTCAAGTCGCGGGTCTCGGCCAAAGATCGAGGGCG
 TGCAGAAAGTGAACAAGGCTGGGATGGAGAAGGAGAAGGCCGAGGAGAAGCTGGCCGGGGAG
 GAGCTGGCCGGGGAGGAGGCCCCCCAGGAGAAGCGGAGGACAAGCCAGCACCGATCTCTC
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAAGGGGGAGAGCGCAGAGGACAAGGAGCAG
 AGGAGGTTCGGGACTCGGAGGAGGGGCCAAGGTGTGGCTCCTCTGAAGACCTGCACGACG
 GTACGGGAGGGTCCCGACCTGGACAGGCTGGGAGCGACCGGAGGAGCGGAGGAGGGCAGC
 GGGGGACTCGGAGGCCCTGGACGAGGAGAGCT**TGA**CGCCGCGGGCAGCCAGGCCAGCCCCCG
 CGAGCTCAGGCTGCCCTCTCCTTCCCCGGCTCGCAGGAGAGCAGCAGAGAAGTGTGGG
 GAACGCTGTGCTGTTGTATTGTTTCCCTTGGGTTTTTTTTTCTGCCTAATTTCTGTGATT
 TCCAACCAACATGAAATGACTATAAACGGTTTTTTAATGA

FIGURE 174

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDERD
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSQDFTPEKKA AVRPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVSKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRERADRGAEARGSGGSSGD
ELREDDEFPVKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQQAQKPVKVERTKRSEGFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDS PDVKRC
LNALEELGTIQVTSQILQKNTD VVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEKLAGEEELAGEEAPQEKAEDK PSTDLSAPVNGEATSQKGESAEDEKEH
EGRDSEEGPRCGSSEDLHDSVREGPD LDRPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTTCTCCTGGATCTTCAACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAATTA
 ATACCACTTTGAAAGAGACATTTGTTTTTCATC**ATGA**ATGCTAATAAGATGAAAGACTTAAGCCAGAGGCCAAGA
 TTTTCACTTTTCTCGCTTTGATGATGCTAAGCATGACCATGTTGTTCTTCCAGCTCATCTGGCATTCTGAAGCA
 AAAATTCCAAAGACTCAAGCTTAACCTACAAAGACTTGCCTGCTTCAAATAGCTGTATTCCTTTTGGGTTCTATC
 AGAAGGACTGGATTTTCAAATCTTCTCTTAGATGAGGAAAGAGGCCAGGCTGCTCTGGGAGCCAAAGACCACAT
 CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTAAGAAATTTATTGGCCTGCTGCAAGAGGAAAGCGGTGGGA
 ATTTATGTAATTTAGCTGGGAAAGATGCCAATACAGAATGTGCAAAATTCATCAGAGTACTTCAGCCCTATTAACAA
 AACTCACAATATATGTGTGGAACTGGAGCATTTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA
 GGATATTATATTCAAATAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTTCGATCCTCAGCAGCC
 TTTTGTCTCAGTAATGACAGATGAGTACCTTACTCTGGAACAGCTTCTGATTTTCCCTTGGCAAAGATACTGCATT
 CACTCGATCCTTTGGGCTACTCATGACCACCACATACATCAGAATGACATTTACAGAGCACTACTGGCTCAATGG
 AGCAAAATTTTATGGAATCTTCTTCATACCAGACCTACAATCCAGATGATGATAAAATATATTTCTTCTTTCG
 TGAATCATCTCAAGAAGGCGATACCTCCGATAAAACCCTTTCTCGAGTTGGAAGAGTTTGAAGAATGATGT
 AGGAGGACAACCGAGCTGATAAACCAAGTGAACGACTTTTCTTAAGGCCAGACTGATTGCTCAATTCCCTGGAAG
 TGAATGGGCGAGATCTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCAAGAGATGAAAGAAATCCTGT
 AGTATATGGAGTCTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTGTGTGATAGCATGGCTGACAT
 CAGAGCACTTTTAAATGGTCCATATGCTCATAAGAAAGTGCAGACCATCGTTGGTTCAGATATGATGGGAGAT
 TCCTTATCCAGGCCCTGGTATGCTTCAAAGCAAAACCTATGACCCACTGATTAGTCCACCCGAGATTTTCCAGA
 TGAATGTCATCAGTTTTCATAAAGCGGCACCTGTGTGATGTATAGTCCGATATACCAGTTGCGAGAGGCCAACGTT
 CAAGAGAAATCAATGTGGATTACAGATGACACAGATAGTGGTGAATCATGTGATCTGCAAGAGATGGCCAGTAGCA
 TGTATATGTTCTTGAAGCAGACATTTGGAATGTGCTCCTCAAAGTGTGTCAGCATTTCAAAGGAAAATGGAAATATGGA
 AGAGTGTGCTGGAGGATTCGAGATATTCAAGCACTCATCAATCATCTTGAAGCATGGAATTTGCTCTGAAGCA
 GCAACAAATGTACATTTGGTCCCGAGATGGATTAGTTAGCTCTCCTTGCAAGATGCGACACTTATGGGAAAGC
 TTGCGCAGACTGTTGCTTGGCAGAGACCCCTACTGTGCTGGGATGGAAATGCATGCTCGATATGCTCCTAC
 TTCTAAAGAGGAGAGCTAGACGCCAAGATGTAATAATGGCGACCAATCAACCAGTGTCTGGGACATCGAGACAG
 CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATATCC
 TAAATCCCAACAGCACTATTAAATGGTATATCCAGAGGTGAGGGATGAGCATCTGAGAGGAGTTGAAGCCGCA
 TGAAGAATCATCAAAACGGAATATGGGCTACTGATTGGAAGTTTGCAAGAAAGGATTTCTGGGATGTATTATCTG
 CAAAGCCCAAGAGCACATTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCTATTGAGAATGAACAGATGGA
 ABAATACCAAGAGGCGAGAGCATGAGGAGGGGCAAGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA
 CTACATCCAAATCCTTAGCAGCCCAAACTTCAGCCTCGACCACTACTGCGAAGAGATGTGGCAGAGGAGAAAGCG
 GAGACAGAGAAACAGAGGGGCCCAAAAGTGGAAAGCATGCAAGGAAATGAAGAAGAAACGAAATCGAAGACATCA
 CAGAGACTGGATGAGCTCCTTAGAGCTGTAGGCCAGT**ACT**TTTTCTACTTAATTTAAAGAAAGAAATTCCTTACC
 TATAAAAACTTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTGTCAAAGG
 CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAAATTCATTGAAACAGATTTT
 CCAAGAACAAATCTTGCACAAGCAAGTATAAGAAATATCTTAAAAATAGGGGGTTTACAGTTGTGAATGTTTTA
 TGTTTTGAATTTTGAATTTATTTGTCATGTAATAGTTGAGCTAAGCAAGCCCGAATTTGATAGTGTATAAGGT
 GCTTTTATCCTCGAATGTCATTAAGCATGGAATTTACCATCGAGTTGTGCTATGTTCTTATGAACAGATATAT
 CATTCCTATTGAGAACCGACTACCTTGTGGTAGGGAATAAGAGGTACAGACAAATTAAGACAACCTCCCATATC
 AACAGGAACCTTTCTCAGTGAGCCATTCTACTGGAGAAATGGTATAGGAATTTGGAGAGGTGCATATTATTTCTTC
 TGGCCACTGGGGTTAAATTTAGTGTACTACAACTGATTACTGGAAGGGCAGCTAATGTTTCCCCAGGATTTCT
 ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAGTTGGTGCTTAGTTATGTTTATAGATATATACTAA
 GCTCTAGGAGGACGAATGCTTAAATACTTTAATAAGATATGGGAAAAATTTTAAATAAAACAGGAAACAA
 TAAATGATGATTAATGCATCTGTGGGAAGGCATGAGATGGGATTTGTAGAAGACAGGAAGAAAGACGCCAT
 AAAATCTGGCTTTGGGAAAACTCATATCCCCATGAAAAGGAAGAACATCAAAAATTAAGGTGAGATGATGTAA
 TGGAGCTCTTTCTACTAGGTTATAGTAGCTGCCAATTTGTAATTCATCTGTTAAAGATCTGATATTATTTCTTTAGC
 AACTGCTAGCAAAATCTGAGGAACATAAATCTTTCTGAAGAAATCATAGGAAGATGACATCTTTATTTATAAC
 AATGATATTTCAGTATATATTTCTCTCTTTTAAAAAATTTATCATCTGTTATATTTCTTTTACTGCT
 CTTTATTTCTCTGATATATTGGATTTTGTGATTATATTTGAGTGAATGAGAAACATATATACACACAGA
 GAATTAAGAAATGACATTTCTGGGAGTGGGATATATTTGTTGAATAACAGACAGTGTAAATTTTAAAC
 AACGGAAGGGTTAAATTAACCTTTTGACATCTTCACTCAACCTTTTCTCATTTGCTGAGTTAATCTGTTGTAATT
 GTAGTATTGTTTTGTATTTAACATAAATAAGCCTGCTCATGTT

FIGURE 176

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLKITYKDLLLSNSCIPFL
 GSSEGLDFQTLILLDEERGRLLLGAKDHI FLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
 NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRCLKPFD
 PQQPFASVMTDEYLYSGTASDFLGKDTAFTRS LGPTHDDHHYI RTDISEHYWLN GAKFIGTFF
 IPDTYNPDDDKIYFFRESSQEGSTSDKTI LSRVGRVCKNDVGGQ RSLINKWTTFLKARLIC
 SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP
 YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
 AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVISKEKWNMEEVVLEE
 LQIFKHSSIIILNMLS LKQQQLYIGSRDGLVQLSLHRCDTYGKACADCC LARDPYCAWDGNA
 CSRYAPT SKRRARRQDV KYGDPITQCWDIEDSISHETADEKVI FGIEFNSTFLECIPKSQQA
 TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCYCKAQEHTFIHTIVKLT LN
 VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRQRN
 KGGPKWKHMQEMKKKRNRRHHRDLDELPRAVAT

Important features of the protein:

Signal peptide:

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTCATCCTGGAGCATGCCACCOCGGGGGAGCAGA
CAACCTCCCAGGTAAAGCTGGGAGCAAGACCTGAAGCTGTTCCTTCAGGAGCCTGGTGTATTTTCCCCACCCCA
CTCAGCAGTTTCAGCCAGCAGGGGACTGATCAGGTGTGTCTCTGGAGTGGGAGCACAAGGCGCTGGCTGGCAAGA
GTGGCCTGGGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCCGTGACTACAAGATCCAGAACCCTGGGCATC
GGGTGAGTGGGGGGGACAGGTTGTCATGTGCACCTTCTGTCTCAGCAAGAGAGGCTGAGAGAGGGGATCTTGG
AGCCATTGAGGCTGTCACTGAGGCTACAGAGGGGAGGGAAGGATATTTAAAGTAACAGTGTGGCACAATAGTTAA
GAGCAGAGTTTGGAGCTAGACCGACATAGGTTCAAATTTCTTCTGTTCTTCTAGTTCTGTAGGCCCTAGGT
AGGGAGTGACTTTAACTCTCTGGACTTCAATTTCTCTCATCACTAAAGTAGGGCCAATAATAGCACCACCTCAT
AGGGAAGATTAAATGACATAATGTATGTCAATGCAACTAGCAAAAGTACCAAGTCCCATAGTCAAGTCATGCCCCACAG
TATTTTCCACCACCCTGTTCTCTGCCTTCCCAACAGGTAAGTCAACAGCTGGAGGACAGAGGCGGACAGAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGGACATCCGCGGGGACAGGTGAGCC
AGGTGAAGGGGCTGCCCGCTGGCCCTGCTCAGAGGGGCTGCCTTAGATGTGGAGCGCTGGCTGAAGCAGGCCA
TGACCAGGCCCAGGATGAGGTGGAGCAGGAGCGGGCTCAGTGAGGCTCGGCTGTCCAGAGGGGACCTCTCTC
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGGCTGCC
CCCAAGCCTGGCCACAGGGGCTCCCTGCCCTGCACAGCTGGTATTTCCGCTCAGCAGGGGCTGAGAGT
AGCTGACATCACAGGAGGCTGAGTGGCTGGAGGTCATAGAGGAGGGAGATGCTGACGAATGGTCAAGGCTCGGA
ACCAGCAGCGCAGGTAGGATTTGTCTGAGCGATATCTCAACTCCCGGAGCTCTCCCTCCGACGAGGACGAGC
AAGACGATGACAAATCCCTGCGGGGACAGGCCACAGCATTCTGGCACAGGCGCTGTACAGCTACACGGAGCAGCC
GTCTCAGAGGCTGAGCTTCCCTGAGGGGGCACTCATCCGCTGCTGCCCGGGGCCAAGATGGAGTAGATGACG
GCTTCTGGAGGGGAGAAATTTGGGGGCGTGTGGGGTCTTCCCTCCCTGCTGTGGAAAGAGCTGCTTGGCCCC
CAGGGCCACCTGAATCTCTGGCCCTGAACAGATGCTGCGCTCCCTTCTCTCTCCAGGCTTCTTCCCACTGCAC
CTACCTCTGTTGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAGAGCCCTGGACTTCCCTGGGTTCTCGG
ACATGATGGCACCCTGCACCTCAGGCGGATGCGTCCACCACCTCCCGCGGGCTAAAGCCCCGATCTCTGGCCACC
CAGATCCCTTCACTGCAAGGCCAGGGAAGCCTTGACCCCAAGTATGCTGTCTGCTTCACTTCTCAAGCTGTGAGA
CCACACCATCAATGATCAGAGACAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCTCACTCCAAGGT
GGAAACTTGGCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTCCCATTTCTTATCATCTTAGGACC
GGAACTACTACCTTCTCTCTGTATGACCTTATCTAGGTTGGTGAATGCCTGAATCTCTGGGGCTGGAAACC
ATCCATCAAGGTCCTAGTAGTTCTGGCCACCTCTTCCCAACCTGGCTCCATGACCCACCCACTCTGGATG
CCAGGTCCTGCGGTTGGCTGGGGAGAGGAACAGGCTTGGGAATCAGGAGCTGGAGCCAGGATGCAGAGCAG
CTGTAATGGTCTGAGCGAATTTATTGACAATGAATAAAGGGCAGGAAGGCCAGGCCAGGGCTTGGCCCTTTGTG
CTAAGAGGGGAGGGGCCCTACGTTGCTATTGCTTTAGGGGCCACACCGGGCAGGGGCCCTGCTCCAGCTGCCAC
GCTCTATCATATGAGGCGAGGTGTGGGGAAAGCGGGGACAGGCGCTGTGCAGGCGAGGGAGAAGGAGAAGAC
TGAGGGGCTGTGACCTCTCTGAGGCCCCAGGCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC
AGCTGGGGGCACTGCTCCAGTGGAGGGGAGGGCTTTCAGGCCACCCACCCCTGGCCCTGCCAGCTGGTAG
TCCATCAGCACAATGAAGGAGACTTGGAGAAGGAGAATAACACTGTTGCTTCTGTTCAAGCTGTGTCCAGC
TTTTCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGATTTATAGCAAAAGCTAAGCCTGC
AGTTTACTCTGGGGTTCAGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTTC
TTTAGGCTCAGGCACTCACTCATACTCCTGCTCCTGTGTAGAGACACTGAGAGAAAGGGGAGGGG
TCAACAATGAGAGGACAGGATAGTCTCATCAGTGCCCGCCAGAGTAGAGACAATAAGAGCCAGCCAGTGGC
AGTCCCGCTGTGTTTTCTACCTGGTGATCAGAAGTGTCTGGTTGCTTGGCTGCCATTGCTCTTGTAGTGG
GCAGGCTGGGCTGGGCCCCCTCCCGGCCCTCAGTGTGGCTGTGAGAGAGCTCTGGGGTTCCCTTCAAGT
CAGAGGGGTTAGGCTGCTGCTCCTGAGTCTCCATTCTGTACTGGGGGCTCAGCTAGGACCTGGGGCTGGGCC
TCTCAGGGGCAAGCTCTTCAATGGCAGGCACTCCTGCCTTGGGCTGCCCTCCCGACAGCCCTGACACCCGCT
GGTCTGTCTCCCAACAGAGGCCAGCTCTGTCTGTGGGGAGCCATCAGGTTGTCTGAGTCTCATAGGCTG
TCTCAATGTGTGTACCCGGAACCTGGGAGGGAGGGAACACTGGGTTTAGGACCAAACTCAGAGGCTGTTGT
GCCCTCCCTCTGACCAGGAGACTCTGAGTTTGGTGCTACTTCCCTCTAGCTAGGGAGGGCTCTCTC
AGATTGTGGGCACTGTGTAGCCTGACTTCTGCTGAGCTCCAGTCCAGGAGGAAGAGCCAGGCCCACTT
TTGGGATCAGGTGCTGATCACTGGGCCCCCTACCTCAGCCOCTTTCCCTGGAGCAGCTGCCACGCCCA
CAGAGAACACAGTGGTCTCCCTGTCCGGGGGCGCTTTTCTCTCTGGAGCTCCCTGACGACAGATGGAG
GCTCTGTGCTGCGCTCAATGGATGTCAGAGGGCTGCAGAGCCCAAGTGCATGTGTGATGTGAGGGGGGGCT
CCTCTCGAGGCTGAGTGGCATCCACATGGACAGCAGGAGGAGGATGAGGATGAGTATTTCAATTTCCCT
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TTTCTGTCTTATTAATAACTCAATTAAG

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></usr/seqdb2/ssct/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAAARLALLQGAGLDVERWLKPMATQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAQALATRALPCPAHVVFYQAGREDELTTITEGEWLEVIEEGDADEW
VKARNQHGVEGVFVPERYLNFPDLSLPESSQVDSNPNCGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVQFVPSLLVEELLGPPGPELSDPEQMFLPSPSPFS
FSPPAATSLVDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPADPGHDPDLIT
```

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGACAGAGGAGGAAAGACAGAGACAAAGGCACAGCGGAA
 GAAGCGCAGAGACAGGGCAGCAGCAAGAAAGCCGCCACAGAGAGTCTTACAGAGAGGAGAGGCGAGAGAAAGCTGCAGA
 AGACACAGGCGAGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAGGCCAGACCCCTGG
 GCACCTCTCCCAAGGCCAAGGACTAAGTTTCTCCATTTCCTTTAACGGTCTCAGGCCCTCTGAAAACTTTGCC
 TCTGACCTTCCGAGGAGTCCAAAGCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGAGTGTGGAGGACTTGGT
 GCCCTAGACGGCTCAGTCCCTCCAGCTGCAGTACAGTGGCAATGCCAGAGGCTCGCATCCGCGGAGGGG
 CTTGGCAGGGCGCTGGCTGTGGGGAGGCCAACCTGCCCTCTGCTCCCATTTGTGCCGCTCTCTGGCTGGTGTG
 GCTGCTTCTGCTAGTGTGGCTCTCTCTGCTGCCCTCAGCCGGCTGGCCAGCCCCCTCCCGGGGAGGAGGAGAT
 CGTGTTTCCAGAGAGCTCAACGGCAGCGTCTCGCTGGCTGGCGGCCCTCCGAGGCTGTTGTGGCGCTTGCA
 GGCTTTGGGAGAGCGTGTCTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCAGGGGCTGACAGTGCAGTA
 CCTCGGCCAGGCGCTGAGCTGTGGTGGAGCAGAGCCTGGCACTACCTGACTGGCAACCATCAATGGAGTCC
 GGAGTCCGTTGGCATCTCTGCACCTGGGATGGGGAGCCCTGTTAGGCGTGTACAPATAGCGGGGGCTGAATCCA
 CCTCCAGCCCCGGAGGGAGGCCACCTAACTCTGCTGGGGACCTGGGGCTCACATCTCAGCCGGAAGAGTCC
 TGCCAGCGGTCAAGTCCCATGTGCAACGCTCAAGGCTCCTCTTGAAGCCCCAGGCCAGACCCGAAGGCCAA
 GCGCTTTGCTTCACTGAGTAGATTTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCTTCCAGCGTGC
 GGGGCTAAAGCGCTACCTGTCAACAGTGTGACGAGCAGCAGCCAGGCCCTCAAGCACCCAGCACTCCGCAATCC
 TGTCACTTGGTGGTACTCGGCTACTGATCTCGGGCTCAGGCGAGGGGGCCCCAAGTGGGGGCCAGTGTGCT
 CCAGAACCTCCGCACTCTCTGCTGGCAGCGGGGCCCTCACACCCCTGAGGACTCGGCGCTGACCACTTTGA
 CACAGCACTTCTGTTTACCGCTCAGGACCTGTGTGAGTCTCCACTTGGCAGACGCTGGAGTATGGCTGATGTGGG
 CACGCTCTGTGACCGCTCGGAGCTGTGCATTGTGGAGGATGATGGGCTCAGTGGGCTTCACTGTGCTGTCA
 TGAATCGGTCATGTCTTCAACATGCTCCATGACAACCTCAAGGCCATGATCAGTTTGAATGGGCGTTTGGACG
 CTTCCGCAATGTCATGGCCCTGTGATGGCTCATGTGGATCTCAGGAGCGGCTGGTCCGCTCAGTGGCCGCTT
 CATCACTGACTTCTCGGACATGGCTATGGGCACTGTCTTAGACAAACAGAGGCTCCATTGCATCTGCTGTG
 GACTTTCTCGTGGCAAGCATGATGCTGACCGCAGTGGCCAGTCACTTCGGGCGCCGACTGAGCCGCTTGTCC
 ACAGCTGCCCGCGCTGTGCTGCCCTCTGGTGTCTGTGCCACCTCAATGGCCATGCCATGTGCCAGACAAACA
 CTCGCCCTGGGCGCATGGCACAACCTCGGGGCCCGCAGCGGCTGATGGTGGTCCGCTCCACATGGGACCA
 GCTCCAGGACTTCAATATTCACAGGCTGGTGGCTGGGTCCTTGGGGACATGGGTTGACTGCTCTCGGACCTG
 TGGGGTGGTGTCCAGTTTCCTCCCGAGACTGCACAGGCCCTGTCCCGGAATGGTGCCAGTACTGTGAGGG
 CCGCGCTACCGGCTTCGCTCTCTCAACACTGAGGACTGCCCACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA
 GTGTGCTGCCACAAACCCGCAACCGACCTCTCAAGAGCTTCCAGGGCCATGGACTGGGTTCTCGTACAC
 AGGCGTGGCCCCCAGGACAGTGCAAACTCACTGCCAGGCCCGGGCACTGGGCTACTACTATGTGCTGGAGCG
 ACGGTTGGTAGATGGGACCCCTGTTCCCGGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATCCATGCTGG
 CTGTGATCGCATATTGGTCCCAAGAAGAAGTTTGACAAGTGCATGGTGTGCGGAGGGGACGGTCTGGTGTGAC
 CAAGCAGTCAGGCTCCTTCAGGAATTCAGGTACGGATACAACATGTGTGTCATATCCCGCGGGGGGCCACCA
 CATCTTGTCCGGCAGCAGGGAACCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
 TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCGCAGATGTGTTACTGCTGGGCACTGACCTTGGCCTA
 CAGCGGGGCACTGCAGGCTCAGAGCACTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT
 AGTGGCTGAGCAACCCAGGACAGCAGCTCCGATACAGCTTCTGTGCGCCGCGACCCCTTCAACCCAGC
 CCCCCTCCCCAGGACTGGCTGCACCGAAGACAGATCTCGAGATCTTTCGGCGGCGGCCCTGGGCGGGCAG
 GAAATACACTCACTATCCCGGCTCGCTTCTGGGCACCGGGGCTCGGACTGTGGGAGAAAGAGAGAGCTT
 CTGTGCTGCTCATGCTAAGACTCAGTGGGAGGGGCTGTGGGCTGAGAGCTGCCCTCTCTGTGCCCTAAT
 GCGAGGCTGGCCCTGCCCTGGTTTCTGCCCTGGGAGCAGTGTGGGTTAGTGGATGGAGGGGCTGACAGAC
 AGCCCTCCATCTAAACTGGCCCTCTGCCCTCGGGGTACAGGAGGGAGGGGAGGAGGAGGAGGCTGGGCG
 CAGTGTGTTATTATTATTATTATTATTACTTTATTATAGCACAGGGAAGGGGACAAGGACTAGGCTCTGGGGAA
 CTTGACCCCTGACCCCTCACTAGGCTCACCCTGGGCTAGGAAATCCAGGCTGGTGGTGAATAGTATTAAGTGGT
 TGTGATTTGGT
 TTTCTGAAATTTTATTTTGGGAAAGAAAGTCAAGGCTAGGCTGGGCTTCAAGGAGTGAAGGATTTCTTT
 TTTTCTTTCTTTCTTTCTTTCTTTCTTTTGTGAGACAGATCTCGCTCTGTGCCCGAGCTGGAGTGAAGT
 GCATATCTCTGGCTCAGTGCATCTCCGCTCCCGGTTCAAGTATTTCTCATGCTCAGCCTCTCGAGTATGCTG
 GGATACAGGCTCTGCCACCCGCCAGCTAATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
 ACCAGGCTGGATGATTTCAGCTCACTGCAACCTTCGCCCTGGGTCAGCAATCTCTCGCTCAGGCTCC
 CGAGTACCTGAGATTATGCACTACCACTACCACTGCGGCTAATTTTGTATTTTGTAGTAGAGAGGGGTTTCAC
 CATGTTGGCAGCTGGCTGTGCAACTCTGACCTTAGGTGATCCATCGCTCATCTCCCAAGTGTGGGAT
 CAGGCTGTGAGCGACCTGGCTGGCCAGCCCACTAATTTTGTATTTTGTAGTAGAGAGGGGTTTCACTATGT
 TGGCAGGCTGCTTGAACCTGCTGACCTCAGTAACTGACCTGCTCGGCTCCCAAGTGTGGGATACAGG
 TGTGAGCCACCGCCGGTACATATTTTAAATGAATTTACTATTTATGTGATCCTTTGGAGTCAGACAG

FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
 FPEKLNQSVLPVPGSGAPARLLCRLQAQFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGASP
 GTYLTGTINGDPESVASLHWDDGALLGVLYRGAEHLQPLEGGTPNSAGGPGAHILRRKSP
 ASGQGPCMNCVKAPLQSPSPRRRAKREASLSRFVETLVVADDKMAAFHAGLKRYYLLTVMAA
 AAKAFKHPSIRNPVSLVVTRLVILVILSGEEGPQVGPSSAAQTLRSFCAWQRLNTPEDSGPDHF
 DTAILFTRQDLGCVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHD
 NSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSAREFITDFLDNGYGHCLLDKPEAPLHL
 PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
 PAQACMGGRCLHMDQLQDFNIPQAGGWGFWGFWGDCSRTCGGGVQFSSRDCTRPVPRNGGKY
 CEGRRTRFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSPFGPMDWVPRYTGVPAPQDQCK
 LTCQARALGYYYVLEPRVVDGTPCSPDSSSVQVQGRCIHAGCDRIIGSKKFKDKCMVCGGDG
 SGCSKQSGSFRKFRGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
 MPSPTRDVVLPGAVSLRYSGATAASETLSGHGFLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
 PSTPRPTPDWLHRRRAQLLEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
 172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
 582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
 AAGAAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT
 AATTGTCCTGTTTTGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
 TGGAGCACACTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAATTGATCCTGTG
 ACCGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
 TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAATGTTTTATCAAACTCAGA
 TTAAAGTGATTCTGAATTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTTCTTAAAAATTCAAAAATCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
 AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAATGACTATACTG
 AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTATTGTGTATTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCGCTGTGTGAACCTTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTATCATGCCTTGTAACCTGGTGGGTGGCCC
 GCATGCTGGGGAGGGTCT**TAA**TAGGAGGTITGAGCTCAAATGCTTAAACTGCTGGCAACATAT
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
 CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
 AAAAAAAAAAAAAAAAAA

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKT
QIKVIPEFSEPEEEIDENEIITTTFFEQSVIWPVPAEKPIENRDFLKNSKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEELPINDY
TENGIEFDPMLDERGYCCICYCRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGACCC**CATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
 GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCAGGCGCGTGCTCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT
 GCGCCTGCGCCGTATCGGGATGAAGTGACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
 ACCTTTGCCATCCTCGGGGACCCCTCTTCATCCTGGCCGGCCTCCTGTGCATGTTGGCCGT
 CTCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCTGCTTTGCCTGTCTGCCAGGACGAGGCACCCACAGGCCCTACCAGGCCCGCC
 CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTATTATATATAT
 TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

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FIGURE 184

MASTAVQLLGFLLSFLGMVGTLLITLPHWRRTAHVGTNILTAVSYLKGLWMECVVHSTGIY
 QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTTPAKTTFAILGGTL
 FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLCLSCQ
 DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

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FIGURE 185

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCGGCAGGGCGGGCGGCCAGGAT**CATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAAGCTTCACCGAATGCAGGCCCTATTTCACCATCCTGGGACTTCCAGC
 CATGTGTCAGGCAGTGCAGAGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCTCC
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
 GTCTGTGTTTGCCAAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGTGGGATGGTGCAGACTGTTCCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGTG
 GGCTGGGTCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
 CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCCTCAGGCCACAGTGTG
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAAACAAG
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCAGCTA
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCACAAA
 AACAAAGGAGATCCCATCTAGATTCTTCTTGCTTTGACTACAGCTGGAAGTTAGAAAAGC
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
 TTCTTTTTTTAAATATAAATTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC
 ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAAACCATTGATGATCTA
 TTTCCAGCTTATCCCCAAGAAAACCTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT
 CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCAGCCCATGATCTCGGTTTTCTTACACTG
 TGATCTTAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTG
 CTGTTGACATCTTCTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG
 TCCTCTTTCTGTCGCGGGTCAGAAATGTCCCTAGATGAATGAGAAAATTATTTTTTTTTAAT
 TTAAGTCTAAATATAGTTAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTTGACATTGTCT
 ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAAGTTTCAGAGCTAGCCTG
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCCAGCATTCCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCACAGG
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCCTGCACTCCAGCCAGGTGACATAGCAGGA
 TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCTAGGAAGTAGGTTAAA
 ACTAATTCCTTAA

FIGURE 186

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYSPSKHDYV
```

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG
 GAGTCCAGCTGGCTAAAACATCATCCAGAGGATA**ATG**GGCAACCCATGCCTTAGAAATCGCTG
 GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
 AGAGTGTGCGCCTTCATTGAAAAACAACATCGTGGTTTTTGAAAACTTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
 CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC
 TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTTGCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAAT
 GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTTGTGCAACGAAAAGAGCAGTAGCTACA
 GATACCGATACCTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGT**GTA**GTGTGATGTTTTTTAACTTTACTATAAAGC
 CATGCAAAATGACAAAAATCTATATTACTTTTCTCAAAATGGACCCCAAAGAACTTTGATTTA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAACGTGTCATCAGCTATTATGATTCTATAA
 GCTATTTTCAGCAGAATGAGATATTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTACTTCAAAATGACATTGCT
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATTTGTTTAAAAACAGCTTAGGGATTAATGTCTCCATTTATAATGA
 AGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTG
 TTTTTAGCCTAGGAGTTAGAAATCCTAACCTCTTTATCCTCTTCTCCAGAGGCTTTTTTT
 TTCTTGTTGATTAAATTAACATTTTTTAAACGCGAGATATTTTGTCAAGGGGCTTTGCATTCA
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAAAAATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA
 GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATATAAATAAAGAGCAGAAAAATATGCTTGGTTTTTCATTTGCTTACCAAAAAACAACA
 ACAAAAAAGTTGTCCTTTGAGAACTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATG
 TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTGTGACCATTCTGTTTTAGTTTTACTAAA
 ATCTGTAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAAACTGACAATCCAATTGA
 AAGTTTGTGTCGACGCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTTATACATTTATA
 TTAATAAATTTGTACATTTTCTAATT

FIGURE 188

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCCATGGCCTCTGCCGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTTCATCGGCAACAGCAT
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTGCTGGTGCAGAGCACCGGCC
AGATGCAGTGAAGGTGTACGACTACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTGCGCTTGTGGTCTACCTTGTGGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTACCTCTGGGA
TTGTCTTTGTATCTCAGGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCAAAAGCGGGAGCTGGGGGCCTCCCT
CTACTTGGGCTGGGCGGCCTCAGGCCCTTTTGTGTGGTGGGGGGTGTGTGTGCTGCACTT
GCCCCCTGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCGCTACTCAACATCTGCCCTT
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCTGACGTGGAGGGGAATG
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT
CGTACCTTTTGTCTTCTGCCTCCTGCTATTTTTCTTTTACTGAGGATATTTAAATTCATTT
GAAAAC TGAGCCAAGGTGTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCTTGG
ATGATGGAGCCAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
CAGTCAAGCTATGGAACATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC
TGTCCTCAAGAGTTCTGCTGCTGCTGGGGCTGGGCTTCCCTAGATGTCAGTGACAGCTG
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAATCATCTG
TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCTCCGCTCTGATAAGACG
TCCACCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTTCTGCCCTGCCCCCTCGTCTACCCCTTTACACTCACATTTTTATCAAATAAGCATG
TTTTGTTAGTGCA

FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLALPQDLQAARALCVIALLVALFGLLVLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIRDFYNPLVAEAQKRELASLYLGWAASGLLLGGGLLCCTCP
SGGSQGPSHYMARYSTSAPAISRGPEYPTKNYV
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Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

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FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG
 AGCATCTTCTACCACCTCCGAATTGAACCAAGTCTTCAAAGTAAAGGCAATGGCATTATATCCC
 TTGCAAATTGCTGGGCTGGTTCTTGGGTTCTTGGCATGGTGGGGACTCTTGCCACAACCCCT
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
 TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
 TAGTCTCTTGTGGCTCTCCCGCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
 GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCTCTTCATCCTGAC
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA
 ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCTTGGCTGGGCA
 AGCGCTGCTGTCTCTTCTATTGGAGGGGGTCTGCTTTGTGGATTTTGTCTGTGCAACAGAAA
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTAATGCCTCCTTTTGGCTCCAAGT
 ATGGACTATGGTCAATGTTTTTATAAAGTCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
 GAAGTCTCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
 AATGAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
 GACCCAATCGTGCTCCAATTTTCATATTTCTAAATTCAAGTATACCCATAATCATTAGCAAG
 TGTACAATGATGGACTACTTATTACTTTTGGACCATCATGTATTATCTGATAAGAATCTAAA
 GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDfYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV
```

Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 194

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
```

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><subunit 1 of 1, 85 aa, 1 stop
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><MW: 9232, pI: 7.94, NX(S/T): 0
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```
MKITGGLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIFCPITYLPVCGSDYITYGN  
ECHLCTESLKSNGRVQFLHDGSC
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Signal peptide:

amino acids 1-19

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1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85
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FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
 CGCGGCCCATGGCTGCCTCCCCGCGCGGCTGCTGTCTGGCCCTGACCGGGCTGGCGCTGC
 TCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA
 AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
 ATTCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGACTCGGCCCGAGGTGC
 AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
 ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
 CTATGATGAAGACTCTGCAATTGGTCCCGGAGCCCTACGGCTTTAGGCATGGAGCCAGCG
 TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT
 TCTTCATGTATCTCCTAATGCCTTACACTACTTGTTTTCTGATTTGCTCTATTTTCAGCAGAT
 CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGGTTAAAAACAACATGTAAATGCCTTT
 TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAATAAAGCATTTTGTTAAAAAGA

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FIGURE 196

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FIGURE 197

CGGCTCGAGCCCGCCGGAAGTGCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC
 GGTAGCGCGGCGGGCAAGGCAGGCGCC**CATG**ACCCTGATTGAAGGGTGGGTGATGAGGTGAC
 CGTCCTTTTCTCGGTGCTTGCTGCCTTCTGGTGTGGCCCTTGCTGGGTCTCAACGCACA
 CCCTGAGGGCGGGGACCACTGCCCCAGCCGTGAGGGGAGCCCAACGCCATCCCAGCCAGC
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCAAGCCT
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCAGCGGGTTTACAGCAACACCGCCAG
 CCCCAGACTCCCCGAGGAGCCCTCGTGCTACGGCTGAAATTCCTCAATGATTAGAGCAG
 GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGTAGGCGACGACACCCAGACCCCTGG
 GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
 CCAAATCCCCCTGCCGCGGGGTCGAGCCCGGCCCTCCGGGCTGGAATCGGCAGCCT
 GCTGCTGCCCCGTGCTGCTCCTGCTGTTGCTGCTGCTGCTGGTACTGCCAGATCCAGTACCGGC
 CCTTCTTTCCCTGACCGCCACTCTGGGCTGGCCGGCTCACCTGCTCCTCAGTCTCCTG
 GCCTTTGCCATGTACCGCCCG**TAGT**GCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCTCC
 GGACCTTGCTCCCCGCGCGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG
 CCTCTTCCCGCTGCCCTGGAGCCAGCCCTGCGCCGAGAGGACTCCCGGACTGGCGGAGG
 CCCCGCCTGCGACCGCCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
 CTGGGAGTGGGCTCCTCGGGGTGCGGCATCTGCTGTGCTGCTCGGCCCGGGCAGAGCCG
 GGCCGCCCGGGGGCCCGTCTTAGTGTTCTGCCGGAGGACCCAGCCGCTCCAATCCCTGAC
 AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTCGGTGGGAGGCTGGTGAAGGGGAGCGGGGAG
 GGCAGAGGAGTTCCCCGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTAAAAAAAAA
 AAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLQPSTPTPSQPSAAMAATDSM
 RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSQPEPLVLRLLKFLNDSEQVARAWPHDT
 IGSLKRTQFFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCVLHCHVSTRVGPPNPCCPPGS
 EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

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FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
 ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
 TCAGCTGCACCTCCTCCCCCTCCAAGG**ATG**ACAAAGGCGTACTCATCTATTTGGTCAGCAGC
 TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
 GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG
 AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC
 TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA
 CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGGCATCCACTGCGCAAAAAGGA
 TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACGTTCAGGCCGG
 CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGAT**TGA**AACAGGGTGCGGGTGCACCGTGG
 AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTTCATTCTTCTTCTACTGCCTCCA
 CTTTCATGTTATTTTCTTCCCTTCCCATTTTACAACATAAACTGACCAGAGCCCCAGGAATAAA
 TGGTTTTCTTGGCTTCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTTCTGTCTGTTAT
 TTGTAAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG

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MTKALLIYLVSFFALNQNQSLISRCDLAQVLQLEDLDGFEGLSDWDLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLCNVDCQDLLNPNLLAGIHCARIKRVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRRLR

Signal peptide:

amino acids 1-18

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACC
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTATTATACAAAGGGGGAAAGAAACACCTGAG
 CAGAATGGAATCATATTATTTTTTCCCAAGGAGAAAACCGGGGTAAGAGGGGGGAAGCAATTC
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAACCTTGGGTCCTGTGGTTTTCTGATTGTAAGTGAAGCAGGTCCTTGCACACGC
 TGTGGCAAAATGTCAAGACAGGTTAAGTGACTGGCAGAAAAACTTCCAGGTGGAACAAGCA
 ACCCATGTCTTGCCTGCAAGCTTGAAGGAGCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
 CTGTTGCATTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG
 CAGACTCCAGTTCTCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGCCGATGT
 TGCACCCCTCCCACCACACCCCTGCACCAGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCCTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCTTACCCAGGCCAGAAGGAACCCAGAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTCAAGCTGGACCCAC
 GTGGCCTCCAGAGGACCTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGG
 CACCACCTGTGCTGACAGCAGCACCCTCAGGACAGCCTGCCACAGCCAGCGTGATCTCTG
 TTTCCATGATGAGGCCTGGTCCACTCTCTGCGGACTGTACACAGCATCCTCGACACAGTGC
 CCAGGGCCTTCTCTGAAGGAGATCATCTCTGAGCAGCTCAGCCAGCAAGGACAACCTCAAG
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTAGTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT
 TCATGGATGCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGCTGATAGATGTGATTGACTGGAAGACTTTCCAGTA
 TTACCCCTCAAAGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCTGGAAC
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCATAAGCCCCATCAGGAGCCCTGTG
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC
 TCTTATGTCGCTGCGAGGTGGTGAAAACCTCGAACTGTCTTTCAAGGCCCTGGCTCTGTGGT
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCTCAT
 TCCCCCTCGACAGGAGGCCACCCTGAGGAACAGGGTTTCGATTTGCTGAGACCTGGCTGGG
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCAGAGGCCCTTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTTGCAGCTGCAAAGGAGACTGGGTGTGCGACATTCCACTGG
 TTTCTGGCTAATGTCTACCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAA
 GCTCCACAACACTGGACTTTGGGCTCTGTGCAGACTGCCAGGCAGAGGGGACATCTGGGCT
 GTCCCATGGTGTGGCTCCTTGCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC
 AGGAAGGAGATTCACTTTGGCAGCCACAGCACCTGTGCTTTGCTGTGAGGAGGAGCAGGT
 GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG
 AGAATGGGATGATTGTCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAGAAAAAC
 AATAAAGATTGTACCTGCGTCCGTGTGATGAAAAAGCCCGCAGTCAGGTGGCGATTGTGACCA
 GATAAATGCTGTGGATGAACTGATGTAATGTCAATGTCAGAAGGAAAAGAGAAATTTGGCCAT
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCTTTTGTGTG
 GTGTGCTCCTTGTGTGTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT
 TCACACCTTATTTTCAATTGACTGCTGGCTGCTTA

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTVAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEYSPLLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKKEAPKRDWGADEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDLVLFMDAHCECHPGWLEPLLSRIAGDRSRVSP
VIDVIDWKTQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQNDSDHSPLDQEATL
RNRVRIAETWLGSEFKETFYKHSPEAFSLSKAEKPDCEMERLQIQRRLGCRTFWHFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGLDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQHWDFFQENGMIHVHILSGKCMEEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACACAGCTGAGGAAGACCTCAGACATGGGA
 GTCCAGGATGTGGCTGCGCTGCTGTGTCCACCTCCTCCCTCTCTGGCCACTGCTGTGGT
 TGCCCCCTCCACCCGCTGCTCAGGGCTCTTCATCCTCCCTCGAAGCCCCACGAGCCCCAGCC
 CGCCCCCGGTGTGCCAGGGGAGGGCCCTCGGCCCCACGTCATGTGTGCTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCTCGGGTCCCAAGATCAGCTCGGCAGTCTGCTGGCACTG
 CACCCCCAGCCACCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT
 ATCGTGTGGGCTCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTGTGCCAATCCCGG
 ATTTCTGGACTATGGTTTTGCAGCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGAGAGGACCTGCCACCTGCGGCCATTCT
 CTGTTTCGGGGCCGTGGGGAAGGTGTGGACCCACGCTCTATGTCACAATTACCATCTCCAT
 CATCATTGTTCTCGTGGCCATGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
 GACGCAGACCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGCAGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTCTGGGGGCTTCGGGGACTACCTACCCCCACCC
 TGACCATGAGGAGCCCCGAGGGGACCCGGCTGGGATGCCCCACCCCAAGGGGGCTCCAG
 CCTTCCAGTTGAACCGGTGAGGGGAGGGGCAATGGGATGGGAGGGCAAGAGGGAAGGCAAC
 TTAGGTCTTCAGAGCTGGGGTGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCGAGCGGTGGC
 CTCCCACAGCCCTGGCCCTCCCAAGGGGGCTGGACAGCTCCTCTCTGGGAGGCACCTTTC
 CTTCTCCAGTCTCTCAGGATCTGTGTCTTATTCTGTCTGCCATAACTCCAACCTTGCC
 TCTTTGGTTTTTCTCATGCCACCTTGCTAAGACAACTCTGCCCTCTTAACCTTGATTCCC
 CCTCTTTGCTTTGAACCTTCCCCTTCTATTCTGGCTACCCCTTGGTTCTGACTGTGCCCTT
 TCCCCTCTCTCTCAGGATTCCTTGGTGAATCTGTGATGCCCCAATGTTGGGGTGACGCC
 AAGCAGGAGGCCAAGGGGCGGCACAGCCCCATCCCACTGAGGTTGGGGCAGCTGTGGGA
 GCTGGGGCCACAGGGGCTCCTGGCTCTGCCCCCTGCACACCACCCGGAACACTCCCCAGCC
 CCACGGGCAATCTATCTGCTGCCCTCCTGCAGGTGGGGGCTCACATATCTGTACTTCG
 GGTCCCTGTCCCCACCTTGTGCACTCACATGAAAGCCTTGCACTCACTCCACCTTAC
 AGGCCATTTGCACACGCTCCTGCACCTCTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT
 CATGTTCTCTGCTCACAATTTGCACCTCTCTCTCCACATTTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTCTGCACTTTACCTCTCATGTGCGTTTTCCGGGCTGATGTTGTGGTGG
 TGTGCGGCGTGTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGAGCCCTG
 GTGCTGCTCCAGAGGTGGTGGGAGGTGAGCTGGGGGCTCCTGGGCCCTCATCGGTATGG
 TCTCGTCCCATTCACACCATTTGTTTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA
 TCACCTGAGGGCTCCCCCTGGGAAATGGGGTAGTGAGGCGCCAGACTTCACCCACGCCA
 CTGCTAAAATCTGTTTTCTGCACAGATGGGTTTTGGGGAGTCGCTGTGCACTACATGAGAA
 AGGGACTCCCATTTGCCCTTCCCTTTCTCCTACAGTCCCTTTGTCTTGTCTGTCCCTGGCT
 TCTGTGTGTGCCATTTCTTGGAATTCAGAGCCCCCTGAGCCCTCCCTCCCTCCAGCT
 CCCTTTGGGCTCCCTAACTCCACCTAGGCTGCCAGGACCGGAGTCACTGGTTCAGGGCC
 ATCGGAGCTCTGCTCCAGTCAACCTTCCCTTCCCGGACTCCCTCTGTCTCCCTCCTTT
 CCTCCTCTTCTCCACTCTCCTTTGCTTCCCTGCTTCCCTTCCCTTCCCTTCCCTCCTAGGT
 CTTCCTCTCTCACTGGTTTTTCCACCTTCTCTCTTCTTCTTGGGTGATCATCTGAATTACTGT
 GTGATATATATTTTGTATTATCTTCTTCTTCTTCTTGGGTGATCATCTGAATTACTGT
 GGATGTAAAGTTTCAAATTTTCAAATAAGCCTTTGCAAGATAA

FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
 PGRDGSPGANVPGTPGIPGRDGFKEGEGCLRESFEESWTPNYKQCSWSSLNYGIDLKIA
 ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
 STINIHRSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGG**ATG**
 CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG
 CTCACAGACGATGTTCCACAGAGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
 GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
 CAGCCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAAGGGC
 GGCGGGTCTGCTGGGGCCCGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
 CGTGGTGTCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA
 GGGGCCGCGCCCGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAA

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FIGURE 206

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCIALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCCGTTGGTTGGTGC GCGCGGTGAAGGGTGTGGCGCAGCAGCGTCGTTGGTTGGCCGGCGG
 CGGGCCGGGACGGGC**ATGG**CCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA
 CGGCTGTCTGCATGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATTGTGA
 ACTTCAAGTCTGGTGGGTGGGCGACATCCCCGTGTAGGGGCGCTGCTACCGACTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
 CCGGGTATTTCCTCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC**TAA**GTAGCCC
 CCAGAGGCGCTGGGAGTGTTGCCACCGCCCTCCCTTGAAGTTTGCTCCATCTCACGCTGGGG
 GTCAACCTGGGGACCCCTTCCCTCCGGGCCATTGGACACACATACATGAAAACAGGCCGCAT
 CGACTGTGACACCGCTGTGGCATCTTCCAGTACGAGACCATTCTCTGCAACAACTGCACAG
 ACTCGCACGTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
 GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCAC
 CTGGCTGTATCGGTAGGGCGGGCCGTGGGTTGAGGGCGCACCACTTCCAAGCCTGTGT
 CCGACAGGTCCTCGGCGCAGTGGAAAGTCAAGTGTCCAGGGCCCTCTGAACATACATAAATAAC
 TGGCACAAGTAAGTCCCCCTCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
 GGTGAGTATGTGTGGGCGACAGGCTGGCTCCCTCAGCTCCCACGTCTAGAGGGGCTCCCGA
 GGAGGTGGAACCTCAACCAGCTCTGCGCAGGAGGGCGGTGCAGTCTTTTCTCCCTCAAAG
 GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTCTCTAAAGGGTCCCCATAGGGTCTGGTTCC
 ACCCCATCCCAGGTCTGTGGTCAAGCCTGGGAGGGTCCCTACGATGGTTAGGGGTGCCCC
 ATGGAGGGGCTGACTGCCCCACATTGCCTTTTCAAGCAGGACACGAGCATGAGGTAAAGCCGC
 CTTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT
 AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC
 CTCTGAACCAACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG
 CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCCTCGGGAGA
 AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCTTTCGGACATCCCAGGC
 ACGAGGGTGTCTGGATGTGGCCACACATAGGACCACAGTCCCAGCTGGGAGGAGAGGCCT
 GGGGCCCCAGGGAGGGAGGCGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
 CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGAGCCCCACACTTGGCCAACCTGACCT
 TGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCAAGGCAAC
 GTGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC
 CTAGGACCCCTCTCCGACCCCGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
 GAGGGAATGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGAGAGCTGCGGGA
 TGTGATTAAAGTCCCTGATGTTTCTC

FIGURE 208

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
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><subunit 1 of 1, 157 aa, 1 stop
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><MW: 17681, pI: 7.65, NX(S/T): 1

MAALLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK

ELHLAIPAKITREKLDVATAVYOMMDOLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER

HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

Signal peptide:

amino acids 1-15

Year	Age	Sex	Height (cm)	Weight (kg)	Body Mass Index (kg/m ²)	Waist Circumference (cm)	Hip Circumference (cm)	Waist-Hip Ratio	Trunk Circumference (cm)	Trunk-Hip Ratio
1990	44	M	170	75	25.9	85	100	0.85	90	0.90
1991	45	M	170	75	25.9	85	100	0.85	90	0.90
1992	46	M	170	75	25.9	85	100	0.85	90	0.90
1993	47	M	170	75	25.9	85	100	0.85	90	0.90
1994	48	M	170	75	25.9	85	100	0.85	90	0.90
1995	49	M	170	75	25.9	85	100	0.85	90	0.90
1996	50	M	170	75	25.9	85	100	0.85	90	0.90
1997	51	M	170	75	25.9	85	100	0.85	90	0.90
1998	52	M	170	75	25.9	85	100	0.85	90	0.90
1999	53	M	170	75	25.9	85	100	0.85	90	0.90
2000	54	M	170	75	25.9	85	100	0.85	90	0.90
2001	55	M	170	75	25.9	85	100	0.85	90	0.90
2002	56	M	170	75	25.9	85	100	0.85	90	0.90
2003	57	M	170	75	25.9	85	100	0.85	90	0.90
2004	58	M	170	75	25.9	85	100	0.85	90	0.90
2005	59	M	170	75	25.9	85	100	0.85	90	0.90
2006	60	M	170	75	25.9	85	100	0.85	90	0.90
2007	61	M	170	75	25.9	85	100	0.85	90	0.90
2008	62	M	170	75	25.9	85	100	0.85	90	0.90
2009	63	M	170	75	25.9	85	100	0.85	90	0.90
2010	64	M	170	75	25.9	85	100	0.85	90	0.90
2011	65	M	170	75	25.9	85	100	0.85	90	0.90
2012	66	M	170	75	25.9	85	100	0.85	90	0.90
2013	67	M	170	75	25.9	85	100	0.85	90	0.90
2014	68	M	170	75	25.9	85	100	0.85	90	0.90
2015	69	M	170	75	25.9	85	100	0.85	90	0.90
2016	70	M	170	75	25.9	85	100	0.85	90	0.90
2017	71	M	170	75	25.9	85	100	0.85	90	0.90
2018	72	M	170	75	25.9	85	100	0.85	90	0.90
2019	73	M	170	75	25.9	85	100	0.85	90	0.90
2020	74	M	170	75	25.9	85	100	0.85	90	0.90
2021	75	M	170	75	25.9	85	100	0.85	90	0.90
2022	76	M	170	75	25.9	85	100	0.85	90	0.90
2023	77	M	170	75	25.9	85	100	0.85	90	0.90
2024	78	M	170	75	25.9	85	100	0.85	90	0.90
2025	79	M	170	75	25.9	85	100	0.85	90	0.90
2026	80	M	170	75	25.9	85	100	0.85	90	0.90
2027	81	M	170	75	25.9	85	100	0.85	90	0.90
2028	82	M	170	75</						

FIGURE 209

AGCAGGAGCAGGAGAGGGACA**AATG**GAAGCTGCCCCGTCCAGGTTCATGTTCTCTTATTTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCTCG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCATACTCCA
 TAGCATGGTGCAAAAATTTCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCCGCTGGTAGACAATGAACAACTG
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCGTGTGACTGTGATTGGGTATATCAACAGCG
 TAATTCAGATTTCATCTCTCTCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAACATAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAAATTTTGTGATGGATTCTAAGTGGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**CTGAC**TTCTCTCTTGGAACTACATATGGCC
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACACACACACACGACGCGTGCACACGACGCGCAGCGTGCACAC
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTC
 TTCTTCTCTTTTTAAATTTTCATATCTCTCACTCCCTATCCAATTTCTTCTTATCGTGCAAT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCTGCTCTTTTAAGGTTACCTAAGGGT
 TGAACCTCTACCTTCTTTTATAAGCACATGTCCGTCTCTGACTCAGGATCAAAACCAAGG
 ATGGTTTTAAACACCTTTGTGAAATTTGTCTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACTCATGCTTGGTTAGCATCTCCAACCTCC
 TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSFSGISTDSEVLTHYNITGNTICLFRDVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQKGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVQNE
CDGFLSGKLLKENRESEKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGCGTGGAGGTGCCACCCGGCGCGGGTG
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
GACGCGGCGGCGGCGGCGGCGGACTGCAGTGGCTGGACG**ATGG**CAGCGTCCGCCGAGCCGGG
GCGGTGATTGCAGCCCCAGACAGCCGCGCTGGCTGTGGTGGTGTCTGGCGGCGGCGCTTGG
GCTCTTGACAGCTGGAGTATCAGCCTTGGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAGTCTACTAGTACGACTGGCGGGTTGACC
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTC
CCAAGGCCAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAG
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
TGTCTAGAAAAAGAGAAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
CTGTGGTCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGC
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
AGGGCCAGTCATATATGCACAGTTAGACCACTCCGCGGACATCAGAGTACAAGATTAAAC
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAA**TTAA**GAGAATACCTAGAACATATC
CTCAGCAAGAAACAAAACCAACTGGACTCTCGTGCAAAAATGTAGCCCATTAACCATGT
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTGCATGA
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTGTCTGTTTTTGTACTTTCTTTTC
AGGTCATTTACAATTGGGAGATTTTCAGAAACATTCTTTTACCATCATTTAGAAATGGTTTG
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAA
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCCTTG
AAATGTGTATATCAATTTCTGGATTCTAATAGCAAGATTAGCAAGGATAAATGCCGAAG
GTCATTTCATTCTGGACACAGTTGGATCAATACTGATTAAAGTAGAAAATCCAAGCTTTGCTT
GAGAAGTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTTA

FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKSDASININ
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTYGCSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

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FIGURE 213

GCCGGCTGTGCAGAGACGCC**ATGT**ACCGGCTCCTGTGCAGCAGTGACTGCCCGGGCTGCCGCC
 CCCGGGGGCTTGGCCCAAGCTGCGGACGACGCGGGTCCATCAGCGCGCCGGGCTGCCGCC
 TCTCGGCCACGGCTGGGTGCGGGGCCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGCGGCCCCGCGCAGTCCCCCGGGCCCCGACCCTGAGGCG
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCGGC
 GCCGCCCTGCTCCAGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGACCATGTAAACAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
 CAGGGAACTGGATCTTGATATCCAGTACAACATTATGTTCCCGAATCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTTCTGTACAACAAGATTACTGATTTCCCATTTAAGTGAATTCG
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA
 TGAAGAGAATGTTGCATTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT
 ACTAAATTTAAAACAGAGCAGGAGAATGAAGCCAAATGCCGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGGCGAATTATATTGAGAGAAAAGTTGAAAATCAATTGAAT
 CCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
 ACTTTTGGCTATACCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA
 CTATATGCAGAAAATATTCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTTACAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGTCTGTTTCTCATCTGTAAAGTGAAGGAAGTAAACA
 TGTTTATAAGTAAAAAA

FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVCKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRAR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
 AGGCTGGTGGGAAGAAGCCGAG**ATGG**CGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACT
 GGTGCGCGAGGGGCTGGGGCGAAGGTCGAGAGGGCGAGGCGCTGTGGCAGGTTGGGGCTGCT
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGAGCGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGCGCACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTCGGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
 GTGTCCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAAGAAGGCCAAGAACCCAGGAGCAGAAG
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCTGTTCCCTCATGATGTGAG
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCTCCCTG**TAA**GTCTATTTAAAAACATCGACGATACATTGAAATGTG
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATTCATGCTCACTTGATACGTTATTAGAAACCCAAG
 GAATGGCTGTCCCATCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
 TAAACTGTCCCCAGATCGACACGCAAAAAAAAA

FIGURE 216

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRI PRRP GALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELENTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWYIIIPVVLFLMSGAPDTGGQ
GGGGGGGGGGGSLCCVPPSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCGGGGCGTCCCGCAGACCGGGGCAGCAGGTGTCGGGGGGCCACC
ATGCTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC
 GTCAAGATGCCGGGTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAATCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTTGCCCTCTACAGTCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTG
 GCAAGAATTCTTTGTGCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCTGCTGAGT
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCTTGGCCCTTCGAAACTGGGGGAGAACTATGACC
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCCTCCTGTCGGACCGCCGC
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTATCTTTCATCTTTGCTTCCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGTGTCCTTGTGCTCATCGTCGCTTCTCTCTCTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGTCCGGTGGAGTCTTCATAGCCTTTCTACTATTGAGT
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCTTAGGGCT
 CCTTGTCTCCTCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTACGACATTTGCTCTG
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCCTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTTGAATCCAGCTATCCGGGATTGTACAGATCTCTCTGT
 GACTGACTTTGTGACTGTCTGTGGTTTCTCTGCCATTGCTTTGTGTTTGGGAGGACATGA
 TGGGGTGATGGACTGGAAGAAGGTGCCAAAAGTTCCTCTGTGTTACTCCCATTTAGAAA
 ATAAACACTTTTAAATGATCAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
 LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
 QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
 VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
 VLLGLTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ
 PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLELACGLYFPSMSFLRRKVIPET
 EQAGVLNWFVRVPLHSLACLGLLVLHDSDRKTGTRNMFSCSAVMVMALLAVVGLFTVVRHDA
 ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
 314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGCGCGGGCCGGGCCCTGGAG**ATG**
 GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCCTCGGGCCCA
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCTGGGGACATTCGATACA
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGCAACGGTTTCTTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATT
 CCATCCCAGTCAATGTCAACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
 TGG**TAGA**AAGAGTTTGTCCACATTCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
 AGGAATTTTGCTACTTGGAAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTTGGGCGTTGTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCAGG
 GCCCCAAGGGTGTCTCATGTACTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACT
 CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
 AGTGGTTTAAAGAGCTGGTGTTTGGGGACTCAATAAACCTCACTGACTTTTGTAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

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></usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIHIDYLFQVLSPGDIRIYFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNFFIIQDIALVERGCSFLSKTRVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGHPWAIISIPVNVTSIPTFELLQPPWTFW
```

Signal peptide:

amino acids 1-20

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCCTGCTGTGTGGGCTGGTGGTGA
 TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
 ACTGGGAAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG
 AGGCCAACCCAAAGATGCCACGGACTGGTGTGCCAGACCCATGACTGCTGCTATGACCACC
 TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAGCAGCATACATTGTATGGAT
 TTATCTCAACGCTATTGTTTAATGGCTGTGTTTAATGTGATCTATCTGGAAATGAGGACTC
 CGAATAAAAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

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 11-20
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 31-40
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 841-850
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 861-870
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 881-890
 891-900
 901-910
 911-920
 921-930
 931-940
 941-950
 951-960
 961-970
 971-980
 981-990
 991-1000

FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCgiYKDNnkSSIHCMDLSQRYCLMAVFNVIYLENEDSE
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCCTTCTGGATGGGGGCCAGGGGGGCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACTCACCCGTGGGTGCGTTAGGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAAA

FIGURE 224

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK
LGDSWDVKLGALGGNTQEVTLQFGEYITKVFVAFQAFLRGMVMTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIKFEWNYPLEEPTTEPPVNLTYSANSPVGR

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Signal peptide:

amino acids 1-22

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FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAAC TGGGTGCTCATCACGGGAAGTGTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCC AAT TGGCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTTAGGATCCAGTT
 TTTTTTTTAAACGCGCCCTCCCAACCCCAAAAAAAGTGTAAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATCGGGTGTGGGAT
 TATTGTTCTTGGAGTGTCTGCTGGCTGGCAAGAATAATGTTCAAAATCGGTCCATCT
 CCAAGGGGTCCAATTTTTCTCTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGGCTGTGATGCAACTGGCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAA
 CAATACAAAGCATGGGTTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCCTCAAAAACCTAAGTATAAT
 CAATTAAAGGGCTCAACAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
 TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAAGCTTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCAGGAAGCTGCTGAGTTT
 ACATTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC
 ATGATCAGACTCAAAGAAGCTTCACTGGAGCACAATCAATTTTCAAGCTCAACCTGGCCCT
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAAATAAATCAGTGTGATAG
 GACAGACCATGTCTGGACCTGGAGCTCCTTACAAGGCTTGATTTATCAGGCAATGAGATC
 GAAGCTTTTCACTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA
 TTCCAACAAGCTCACATTTATTTGCTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA
 TCAGTCTTGTCTGGGAATATATGGGAATGACAGAGAAATTTTGTCCCTTGTAAGCTGGCTG
 AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCACTGAAGAAGCTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAGCCGACGTTTAAAGCCCAAGCTTCCCGAGCCGAAGCAT
 GAGAGCAAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCGCCAGAGACCGATGC
 TGACGCCGAGCACATCTTTTCCATAAAATCATCGCGGCGACGGTGGCGCTTTTCTGTCCG
 TGCTCGTCATCCTGCTGTTATCTACGTGTGATGGAAGCGGTACCTGCGAGCATGAAGCAG
 CTGCGAGCGCTCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAT
 TACTCCAGCACCCAGGAATTTTATGTAAGATTATAAACCCCAACACGAGACCGGAGAGA
 TGCTGCTGAATGGGACGGGACCTGCACCTATAACAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTTAAAAGCTGGGAAATAAGTGGTGTCTTTATTGAAGT
 TGGTGAATATCAAGGGAACGATGCCCCCTCCCTTCCCTCTCCTCTCCTCTTGGTGG
 CAAGATCCTTCTTGTCCGTTTTAGTGCATTATAATACTGGTCATTTCTCTCATACATA
 ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAAGCTCCGGTTTAAATATA
 TACCTATTGTATAAGACCTTTACTGATTCCATTATATGTCGCATTTGTTTTAAGATAAACT
 TCTTTCATAGGTAAAAA

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTLLTMLSSAERGCPKGCRCGKMGVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLTIPVRI FQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKEHLHLEHNQFSKLNLALEFRLVSLQNLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVENLQRLNLDNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPPLPPTVGATEPGPETDADAEHISFHKI IAGSVALFLSVLVI
LLVIYVSWKRYPA SMKQLQQRSLMRRHRKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLN
GTGPTCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT
 TAAAT**ATG**CTCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
 TGTTTGCCGCTATTCCAGTTGGTGTCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACACCCCTAATGGCTGGTATATCTGGATCCTCCTGCTGTGGTTTTGG
 TGGCAGCTCTTCTGTGGAGCTGTGGTCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
 ATTGATTCTCACAGGCGACCATGGCAGTTTTTGTCTGTTGGAGACTTGGACTCTATTTATGG
 GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCTGTCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTTGA
 AAAACAACCT**GTGA**TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
 AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTTCATATA
 GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG
 TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
 AACCAAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAACTCTTTC
 CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
 GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
 CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
 CTTTTACAGTAATGAATGTGGCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG
 GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGCCATCAGCAGGGGGACAGA
 CAAAACATCCATCAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
 AAACATCAATAGATATCTAAAAA

FIGURE 228

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
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```
><subunit 1 of 1, 146 aa, 1 stop
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><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTTIGILCLPLFQLVLSDLPCEEDEMVCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

Year	Age	Sex	Location	Length (mm)	Weight (g)	Stomach contents	Notes
1971	1	M	1000 m	100	0.5	1000 m	1000 m
1972	2	F	1000 m	120	0.8	1000 m	1000 m
1973	3	M	1000 m	140	1.2	1000 m	1000 m
1974	4	F	1000 m	160	1.5	1000 m	1000 m
1975	5	M	1000 m	180	2.0	1000 m	1000 m
1976	6	F	1000 m	200	2.5	1000 m	1000 m
1977	7	M	1000 m	220	3.0	1000 m	1000 m
1978	8	F	1000 m	240	3.5	1000 m	1000 m
1979	9	M	1000 m	260	4.0	1000 m	1000 m
1980	10	F	1000 m	280	4.5	1000 m	1000 m
1981	11	M	1000 m	300	5.0	1000 m	1000 m
1982	12	F	1000 m	320	5.5	1000 m	1000 m
1983	13	M	1000 m	340	6.0	1000 m	1000 m
1984	14	F	1000 m	360	6.5	1000 m	1000 m
1985	15	M	1000 m	380	7.0	1000 m	1000 m
1986	16	F	1000 m	400	7.5	1000 m	1000 m
1987	17	M	1000 m	420	8.0	1000 m	1000 m
1988	18	F	1000 m	440	8.5	1000 m	1000 m
1989	19	M	1000 m	460	9.0	1000 m	1000 m
1990	20	F	1000 m	480	9.5	1000 m	1000 m
1991	21	M	1000 m	500	10.0	1000 m	1000 m
1992	22	F	1000 m	520	10.5	1000 m	1000 m
1993	23	M	1000 m	540	11.0	1000 m	1000 m
1994	24	F	1000 m	560	11.5	1000 m	1000 m
1995	25	M	1000 m	580	12.0	1000 m	1000 m
1996	26	F	1000 m	600	12.5	1000 m	1000 m
1997	27	M	1000 m	620	13.0	1000 m	1000 m
1998	28	F	1000 m	640	13.5	1000 m	1000 m
1999	29	M	1000 m	660	14.0	1000 m	1000 m
2000	30	F	1000 m	680	14.5	1000 m	1000 m
2001	31	M	1000 m	700	15.0	1000 m	1000 m
2002	32	F	1000 m	720	15.5	1000 m	1000 m
2003	33	M	1000 m	740	16.0	1000 m	1000 m
2004	34	F	1000 m	760	16.5	1000 m	1000 m
2005	35	M	1000 m	780	17.0	1000 m	1000 m
2006	36	F	1000 m	800	17.5	1000 m	1000 m
2007	37	M	1000 m	820	18.0	1000 m	1000 m
2008	38	F	1000 m	840	18.5	1000 m	1000 m
2009	39	M	1000 m	860	19.0	1000 m	1000 m
2010	40	F	1000 m	880	19.5	1000 m	1000 m
2011	41	M	1000 m	900	20.0	1000 m	1000 m
2012	42	F	1000 m	920	20.5	1000 m	1000 m
2013	43	M	1000 m	940	21.0	1000 m	1000 m
2014	44	F	1000 m	960	21.5	1000 m	1000 m
2015	45	M	1000 m	980	22.0	1000 m	1000 m
2016	46	F	1000 m	1000	22.5	1000 m	1000 m
2017	47	M	1000 m	1020	23.0	1000 m	1000 m
2018	48	F	1000 m	1040	23.5	1000 m	1000 m
2019	49	M	1000 m	1060	24		

FIGURE 229

GAGCGGAGTAAAACTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGCGCT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGAGCCCGCTTATTA
 GCTCTCGCTGCGTCGCCCGGCTCAGAAGCTCCGTGGCGGGCGACCGTGACGAGAAGCCC
 ACGGCCAGCTCAGTTCCTTCTTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAACT
 CCCTCTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG
 ATGAAGAAATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGC
 TTACCTCAAGTTACCATTTTTCAGTCAAGTCTGTTTGTGTGCTTCTTCAGAAATGTTTTTTA
 CAATCTCAAGAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGTATTGGAAGTCAAT
 TGGGGATTGATGTTACTGCACATATCTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
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 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATCGCGATCTGAAAAGAACAAAT
 GCTGTCCCTTCGGATGACATTTGCAACGATTGGTGAAGCTGGAGAACAAGTTGACTATAT
 TGTGTGAATGGCTCAGCAGGCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
 CCACAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTC
 TGCTCCATCCACTGTGGATTATATCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
 AGAGCAATACTTTACAATAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTTCATGGAAC
 TCTAATCTGTACATAAAAAATTTTAAAGTTATTGTTTGCTTTCAGGCAAGTCTGTTCAATG
 CTGTACTATGTCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATT
 ATTTCTATAACACATTTATTTAAAGTATATAACACGTTTTTTGGCAAGTGAAGAATGTTTAA
 TCATTCTGTCAATTTGTTCTCAATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAAATGTG
 CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAATATAATGTTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGATGTATTGATTGCACTATCCTTCAGATAACTGA
 AGGTTAATTATTGTATATTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATTTGGGGCAATTTAATAACAGCATTAAAAAGTT
 GTAAACTCTAATCTTATACTTATTGAAGAATAAAGATATTTTATGATGAGAGTAAACAATA
 AAGTATTCATGATTTTTCACATACATGAATGTTCAATTTAAAGTTAATCCTTTGAGTGCT
 ATGCTATCAGGAAGCACATTATTTCCATATTTGGGTTAATTTGCTTTTATTATATTGGTC
 TAGGAGGAAGGGACTTTGGAGAAATGGAACCTTTGAGGACTTTAGCCAGGTGTATATAATAAA
 GGTACTTTTGTGCTGCATTAAATTGCTTGGAAGTGTTAAACATTATATTATATAAGAGTATC
 CTTTATGAAATTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
 TTAATAATAAGAACTTTAAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAAGCT
 GTATATAGCACAGGAACCCATACTTTGGGTAATCTAGTATAAAACAAATTATACTTTTAT
 TTAATTTCCCTTGTAGCAAACTTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT
 CTCTATAGTAACTGCTTAAGTCAGCTAGCTTCTAGATTTAGACTATAGAAATTTAGATAT
 TGTATTGTTGCTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTA
 TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTCTCTCTCTCTGTA
 CTGTCFACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

FIGURE 230

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR

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Important features of the protein:**Signal peptide:**

amino acids 1-26

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 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1222 1223 1224 1225 1226 1227 1228 1229 1230 1231 1232 1233 1234 1235 1236 1237 1238 1239 1240 1241 1242 1243 1244 1245 1246 1247 1248 1249 1250 1251 1252 1253 1254 1255 1256 1257 1258 1259 1260 1261 1262 1263 1264 1265 1266 1267 1268 1269 1270 1271 1272 1273 1274 1275 1276 1277 1278 1279 1280 1281 1282 1283 1284 1285 1286 1287 1288 1289 1290 1291 1292 1293 1294 1295 1296 1297 1298 1299 1300 1301 1302 1303 1304 1305 1306 1307 1308 1309 1310 1311 1312 1313 1314 1315 1316 1317 1318 1319 1320 1321 1322 1323 1324 1325 1326 1327 1328 1329 1330 1331 1332 1333 1334 1335 1336 1337 1338 1339 1340 1341 1342 1343 1344 1345 1346 1347 1348 1349 1350 1351 1352 1353 1354 1355 1356 1357 1358 1359 1360 1361 1362 1363 1364 1365 1366 1367 1368 1369 1370 1371 1372 1373 1374 1375 1376 1377 1378 1379 1380 1381 1382 1383 1384 1385 1386 1387 1388 1389 1390 1391 1392 1393 1394 1395 1396 1397 1398 1399 1400 1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 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2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613

[illegible]

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652

><subunit 1 of 1, 353 aa, 1 stop

><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLLLAVSGAQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHFTRAGLPAPT
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAAGLGLTHLSLASLQRLPELAPS
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGNTLVPLPEALLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTCTCCCCAGTTCCTTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTAT**ATG**CGTCAATCCCCA
 AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTAC
 GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCC
 TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTATCGCCACAAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGAAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAAATACAGAGCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTTGAAGAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGAACTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAA**TAGG**AGGAAAGTGATGCTGCTGCTAAGAATATTTCGAGGT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCAAACCACCATCTCTTACT
 GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGAT
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTT
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTGCTATTTAATGTATTT
 ATTTTTTTACTTGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
 AGCAGGTGATGTATTTTTATACAGTAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCT
 AGGGGGTTATTCAATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT
 CTTCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAA

FIGURE 234

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEFGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSFLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQA AVVKALG
ELDILLQWMEETE
```

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGGCGTACTGCTGA**ATGT**TCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGCC
 CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
 TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAAGTACCTAGTGAAGGTTGAGATGCAAAAT
 GGAAGGAAAAAGGAACTGGAAGGAAAACCATTCGCATTTCTGGTGTACATCATGCATTTG
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAAATATACAA
 AGAGCAGCACTGGTGAATATGGGAGATTTAACCACTTATGATACAGTGAAACACTACTTGGT
 ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
 TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA
 CGAGATAACAAGGAAGGGGACTTTTGATATAATCATCGACTGACTGCTTGATTGAGGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTT**TAA**

FIGURE 236

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMQGEEAALARLGDGA
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEH
YPLWKSIVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDITVKHYLVLTNPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSSTDCLIQAVQGEFGMSLYKGFLPSWLRMTFWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
 GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC
 TTAAGAAGTAAAA**ATGC**AGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCGAGGTATATTGTTTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGATCCTAAGCCAGAACAGTTGAACCATGCCTT
 TCACACATGTGGTGATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
 TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACCTTA
 TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCT**GA**GATCAC
 TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTATCTCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCCTTACATTTTTATGTTT
 TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTCATTGCATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTATTCCTGAGATTTAGAA
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT
 CTCTCTGGCTGGGCACGGTGGCTCATGCCGTGAATCCAGCACTTTGGGAGGCCGAGGCCGGG
 CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT
 AAAAAACAAAAATTAGCCAGGCATGTTGGTGGGTGCCGTGAATCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTTGAACCCGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
 TGCACCTCTAGCCTGGGGGAGAAAGTGAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
 TAAAAGGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA
 AAAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCC
 AAAGGACTAGTTTGAAAGCTTCTTTAAAAAGAATTCCTCTAATATGACTTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILEFTGWWIMIDAADVYPKPEQLNHAFTCG
 VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
 NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

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FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGGCCCGCAACACTCCGTCTCACCCCTCTGGGCCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGCCAGGGTGGT
 GGTCAGCTGGGTGAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAGCTGACCCCAAGCCACCCCTTACCTGGACAG
GATGAGAGTGTGAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTTTATTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCACCAAGGAGATCCAGGTTAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACTACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCTGTGAAAAACAATGTGGGCAGAGGCCCTAAACATC
 GCCCTGGTGAATGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTA CTCTGG
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGGTGCACTGGTGCTGGTGG
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTTCTCTGACTTG
 GGGAGTTCCTACGCAAAACAACCTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAGCCCCCTTTGAGCAGTTCCTTAAAGAACAGCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGGC
 TGTGGCTCTTCTCAGCCAGGGGCCCTGAAGAAGCTCCTGCTGACTTAGGAGTCAGAGCCCCG
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTCTGCGTGGAAGGTGCTGCAGGTCTTGCACGC
 TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCTCCACAGCACATCTACCCGGAAGACC
 AGCCTCAGAGGGTCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTCTTTTCGTAGGG
 ACTGCTGACGGCTGGTCTGAGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTA
 TTTTGTGCTGTTTTGAAAAAAAAAAAAAAAAAAAA

FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYSFMSKTI RLPRLAASPTKEIQVKYKCGLIKPCP
 ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
 DVMHLVKFLKEIPGGALVLVASYYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
 LRKGS PFQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAGAGGCAGCAAGAGATTTGTCTCTGGGGAT
 CCAGAAACCCATGATACCCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTAGTCTCTAGTCTCAAATCCAGTCCC
 CTGCACCCCTTCCTGGGACACT**TATG**TTGTTCTCCGCCCTCCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA
 GCCTCTTACCCTGAGTGTGGAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT
 GACATTTGACCTGATTTGCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCAGC
 CTTTGACCTGCACAACAATGGCCACACAGTGCAACTCTCTGCCCCCTACCCCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCAGTGGGGTCAGAAAGGATC
 CCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCCTGGCT
 GTCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTCAACCTAAGAG
 AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGTCCCAGATTTCAATTGGAACAGCT
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGCCCTCTAAGCTTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTCATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
 CCTTCTCCTGGCTGTTTATTTCATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGTCTTCACCTCAGCACAAAGCCACGACTGAGGCAT**TAA**ATTCTCTCAGATACCA
 TGGATGTGGATGACTTCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGCTCCTCTCCCTGGACATCTCTTAGAGAG
 GAATGGACCCAGGCTGTCTATCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGG
 GAAGTTTGGGATATACCCCAAAGTCCTTACCCCTCACTTTTATGGCCCTTTCCTAGATA
 TACTGCGGGATCTCTCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGATCAATA
 TATTGGAAATTAAGTTTCTGACTTT

FIGURE 242

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNAQSPIDIQTDSVTFDFDLF
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPPGGSEHQ
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPFCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFAFQAGSSYTTGEMLSLGVGILVGCCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

[illegible]

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
 LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE
 LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGS LPAGGAGVNPATQGT PAGRLPTPSG
 TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

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FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAAGGCGCATTGATGCAGCCTCGCGCGGCCCTCGGAGCGCGGCG
 GAGCCAGACGCTGACCACGTTCCCTCTCCTCGGTCTCCTCCGCCCTCCAGCTCCGCGCTGCCCG
 GCAGCCGGGAGCC**ATG**CGACCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCCTCC
 TGCTGCTCCTGCTGCTGCAGTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATCCGGGTACACCTG
 GGATCCCAAGTCGGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAGCCTTTGAG
 GAGTCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT
 TGGGAAAATTGCGGAGGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
 TCAGTGGCTCACTTCGGCTAAAAATGCAGAAATGCATGCTGTGAGCGTTGGTATTTACATTC
 AATGGAGCTGAATGTTTCAGGACCTCTTCCATTGAAGCTATAATTTATTTGGACCAAGGAAG
 CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTCAGATTACCCAAA
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAA**TA**
AATGCTTTAATTTTCATTTCGTACCTCTTTTTTTATTATGCCTTGAATGGTTCACTTAAAT
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAGCAAAGCTAAATATGTTTACAGA
 CCAAAGTGTGATTTCACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGT
 GGTTTTCAATATTTTTTTTAGTTGGTTAGAATACTTCTTCATAGTCACATTCTCTCAACCTA
 TAATTTGGAATATTGTTGTGCTTTTTTGTCTTTCTCTTAGTATAGCATTTTTTAAAAAATA
 TAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAAT
 AAAAATTATTTCCAACA

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAAASPQRLRGLLLLLLLQLPAPSSASEIPK GKQKAQLRQREVVDLYNGMCLQGFAGV
PGRDGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217